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From: Whiteman, Brian
Sent: Wednesday, January 11, 2006 6:27 PM
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Subject: seq search

10/822873

SEQ ID NO: 10 and 11

- 1) us patents and published us patent applications
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Patent Examiner - Art Unit 1635
United States Patent and Trademark Office
(571) 272-0764

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Searcher: _____
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Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
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WWW/Internet: _____
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QM protein - protein search, using sw model

Run on: January 18, 2006, 19:44:52 ; Search time 23 Seconds
(without alignments)
363.054 Million cell updates/sec

Title: US-10-822-873-11
Perfect score: 551
Sequence: 1 WTGSTIAPTDTYNTATGSL.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	551	100.0	101	2	US-09-033-333-22
2	551	100.0	101	2	US-09-033-428-23
3	551	100.0	101	2	US-09-033-556-10
4	551	100.0	101	2	US-09-614-495-22
5	551	100.0	101	2	US-09-898-883-23
6	551	100.0	101	2	US-09-151-376-11
7	551	100.0	101	2	US-09-814-351-18
8	551	100.0	101	2	US-09-814-292-4
9	551	100.0	101	2	US-09-814-357-18
10	551	100.0	101	2	US-09-875-228-5
11	522	94.7	95	2	US-09-392-822A-8
12	74	13.4	522	2	US-09-549-519-33
13	73.5	13.3	521	2	US-09-489-039A-9549
14	71	12.9	239	2	US-09-934-289A-44
15	71	12.9	277	2	US-09-934-289A-42
16	71	12.9	283	2	US-08-509-024-2
17	71	12.9	283	2	US-09-333-279-2
18	71	12.9	283	2	US-09-072-993C-2
19	71	12.9	283	2	US-09-631-780-2
20	71	12.9	283	2	US-09-334-289A-13
21	71	12.9	283	4	PCT-US96-12374-2
22	71	12.9	284	2	US-09-949-016-7971
23	70	12.7	406	2	US-09-489-039A-8267
24	70	12.7	749	1	US-08-937-931-8
25	70	12.7	749	2	US-09-285-502-8
26	70	12.7	749	2	US-09-709-126-8
27	70	12.7	749	2	US-09-871-385A-8

28 67 12.2 401 2 US-09-489-039A-13241 Sequence 13241, A
29 67 12.2 491 2 US-09-030-335-2 Sequence 2, Appl
30 67 12.2 523 2 US-09-549-519-36 Sequence 36, Appl
31 67 12.2 748 1 US-08-920-234-2 Sequence 2, Appl
32 67 12.2 748 1 US-08-937-931-4 Sequence 4, Appl
33 67 12.2 748 2 US-09-285-502-4 Sequence 4, Appl
34 67 12.2 748 2 US-09-030-335-9 Sequence 9, Appl
35 67 12.2 748 2 US-09-709-126-4 Sequence 4, Appl
36 67 12.2 748 2 US-09-871-385A-4 Sequence 4, Appl
37 67 12.2 761 2 US-09-949-016-10631 Sequence 10631, A
38 67 12.2 799 2 US-09-030-335-4 Sequence 4, Appl
39 66.5 12.1 288 2 US-09-248-796A-14840 Sequence 14840, A
40 66.5 12.1 868 1 US-08-374-834-1 Sequence 1, Appl
41 66.5 12.1 868 1 US-08-644-271-1 Sequence 1, Appl
42 66.5 12.1 868 2 US-09-077-955-1 Sequence 1, Appl
43 66.5 12.1 868 2 US-10-016-283-1 Sequence 1, Appl
44 66 12.0 184 2 US-09-134-000C-3820 Sequence 3820, Ap
45 66 12.0 220 2 US-09-328-714A-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-033-333-22
; Sequence 22, Application US/09033333
; Patent No. 6197293
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,333
; FILING DATE: 02-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-033-333-22

Query Match 100.0%; Score 551; DB 2; Length 101;

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Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60

Qy 61 CLKRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 2
US-09-033-428-23
; Sequence 23, Application US/09033428
; Patent No. 6254862
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; TITLE OF INVENTION: EXPRESSING APHA-PETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-033-428-23

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60

Qy 61 CLKRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 3
US-09-033-556-10
; Sequence 10, Application US/09033556
; Patent No. 6432700
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GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-033-556-10

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CLKRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 4
US-09-614-495-22
; Sequence 22, Application US/09614495
; Patent No. 6436394
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
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/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/614,495
/ FILING DATE: 11-Jul-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/033,333
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Catherine, Polizzi M
/ REGISTRATION NUMBER: 40,130
/ REFERENCE/DOCKET NUMBER: 34802-20007.00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-494-0792
/ TELEFAX: 650-494-0792
/ TELEX: 706141
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 101 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-614-495-22

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CLKRRRARPPIYRPIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRRARPPIYRPIIVLNPNEKIHRLDGLKPCSLLOYD 101

RESULT 5
US-09-898-883-23
/ Sequence 23, Application US/09898883
/ Patent No. 6585968
/ GENERAL INFORMATION:
/ APPLICANT: Little, Andrew
/ Lampareki, Henry
/ Schuur, Eric
/ Henderson, Daniel
/ TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
/ EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORRISON & FOERSTER
/ STREET: 755 PAGE MILL ROAD
/ CITY: PALO ALTO
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304-1018
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/898,883
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/ FILING DATE: 02-Jul-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/033,428
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: POLIZZI, CATHERINE M.
/ REGISTRATION NUMBER: 40,130
/ REFERENCE/DOCKET NUMBER: 34802-30004.00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141 MRSNFOERS SFO
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 101 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-898-883-23

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CLKRRRARPPIYRPIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRRARPPIYRPIIVLNPNEKIHRLDGLKPCSLLOYD 101

RESULT 6
US-09-151-376-11
/ Sequence 11, Application US/09151376
/ Patent No. 6676935
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, D.R.
/ APPLICANT: Schuur, B.R.
/ TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
/ FILE REFERENCE: 34802000221
/ CURRENT APPLICATION NUMBER: US/09/151,376
/ CURRENT FILING DATE: 1998-09-10
/ EARLIER APPLICATION NUMBER: 08/669,753
/ EARLIER FILING DATE: 1996-06-26
/ EARLIER APPLICATION NUMBER: 08/495,034
/ EARLIER FILING DATE: 1995-06-27
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 101
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-151-376-11

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSALMFVCLIIIMWLIC 60

QY 61 CLKRRRARPPIYRPIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRRARPPIYRPIIVLNPNEKIHRLDGLKPCSLLOYD 101

RESULT 7
US-09-814-351-18
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; Sequence 18, Application US/09814351
; Patent No. 6692736

; GENERAL INFORMATION:

; APPLICANT: Yu, De-Chao

; APPLICANT: Li, Yuanhao

; APPLICANT: Henderson, Daniel R.

; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS

; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE

; FILE REFERENCE: 348022001700

; CURRENT APPLICATION NUMBER: US/09/814,351

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/192,156

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence for ADP

US-09-814-351-18

Query Match 100.0%; Score 551; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 6.9e-60;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

QY 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

DB 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 8

US-09-814-292-4

; Sequence 4, Application US/09814292

; Patent No. 6852528

; GENERAL INFORMATION:

; APPLICANT: Zhang, Hong

; APPLICANT: Yu, De-Chao

; APPLICANT: Henderson, Daniel R.

; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING

; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 348022001500

; CURRENT APPLICATION NUMBER: US/09/814,292

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/191,861

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence for ADP

US-09-814-292-4

Query Match 100.0%; Score 551; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 6.9e-60;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

QY 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 9

US-09-814-357-18

; Sequence 18, Application US/09814357

; Patent No. 6911200

; GENERAL INFORMATION:

; APPLICANT: Yu, De-Chao

; APPLICANT: Chen, Yu

; APPLICANT: Henderson, Daniel R.

; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA

; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,

; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION

; FILE REFERENCE: 348022001600

; CURRENT APPLICATION NUMBER: US/09/814,357

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 60/192,015

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence for ADP

US-09-814-357-18

Query Match 100.0%; Score 551; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 6.9e-60;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

QY 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

DB 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 10

US-09-875-228-5

; Sequence 5, Application US/09875228

; Patent No. 6916918

; GENERAL INFORMATION:

; APPLICANT: Yu, D.

; APPLICANT: Henderson, D.R.

; APPLICANT: Schuur, E.R.

; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE

; TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF

; FILE REFERENCE: 348022000900

; CURRENT APPLICATION NUMBER: US/09/875,228

; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 09/127,834

; PRIOR FILING DATE: 1998-08-03

; PRIOR APPLICATION NUMBER: 60/076,545

; PRIOR FILING DATE: 1998-03-02

; PRIOR APPLICATION NUMBER: 60/054,523

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Adenovirus

US-09-875-228-5

Query Match 100.0%; Score 551; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 6.9e-60;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTGSTTAPTDTYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLC 60
QY 61 CLKRRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 11
US-09-392-822A-8
; Sequence 8, Application US/09392822A
; Patent No. 6900049
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: Adenovirus Vectors Containing Cell
; TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
; FILE REFERENCE: CELL-014: 122-1
; CURRENT APPLICATION NUMBER: US/09/392,822A
; CURRENT FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/099,791
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/392,822
; PRIOR FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-392-822A-8

Query Match 94.7%; Score 522; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 APTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLCCKRRR 66
Db 1 APTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLCCKRRR 60
QY 67 ARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 ARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 95

RESULT 12
US-09-549-519-33
; Sequence 33, Application US/09549519
; Patent No. 6673601
; GENERAL INFORMATION:
; APPLICANT: TORDO, NOEL
; APPLICANT: PERRIN, PIERRE
; APPLICANT: JACOB, YVES
; APPLICANT: BAHLOUL, CHOKRI
; TITLE OF INVENTION: CHIMERIC LYSSAVIRUS NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 03495-0188-00000
; CURRENT APPLICATION NUMBER: US/09/549,519
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,501
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Lyssavirus sp.
; FEATURE:
; OTHER INFORMATION: Laginga
US-09-549-519-33

Query Match 13.4%; Score 74; DB 2; Length 522;
Best Local Similarity 35.0%; Pred. No. 1.5;
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Matches 21; Conservative 8; Mismatches 19; Indels 12; Gaps 3;
QY 24 LNLPOVHAFVNDWASLDMWFSIALM-----FVCLIIIMWLCCKRRRARPPIYR 74
Db 437 VMPDVHKLVD---VDLGLPQWLSYALIGATIIAFILICIRICCKKGRNSPTNRP 493

RESULT 13
US-09-489-039A-9549
; Sequence 9549, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9549
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9549

Query Match 13.3%; Score 73.5; DB 2; Length 521;
Best Local Similarity 30.4%; Pred. No. 1.7;
Matches 31; Conservative 16; Mismatches 32; Indels 23; Gaps 8;

QY 4 STIAPTDTYRNTTATGTSALNLPQVHAFVND-----WASLDMWFSI----ALMFVC 52
Db 171 SEVAPTE--MRGKLTGLNEVAIVIGLAAFAINAIIGIINGHLDPVWRYMLLVQAIPAIC 228
QY 53 LII-MWLICCKRRRARPPIYRPIIIVLNPNEKIHRLDGLKP 93
Db 229 LPVGMW-----RA-PESPRWLISKNRHRDEALHILKQIRP 261

RESULT 14
US-09-934-289A-44
; Sequence 44, Application US/09934289A
; Patent No. 6852837
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MBIO98-061CPICN1(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-289A-44

Query Match 12.9%; Score 71; DB 2; Length 239;
Best Local Similarity 35.9%; Pred. No. 1.3;
Matches 14; Conservative 10; Mismatches 11; Indels 4; Gaps 2;

QY 41 MWMF----SIALMFVCLIIIMWLCCKRRRARPPIYRPII 76
Db 164 VMWFLSGSLVIVIVCSTV-GLIICVKRRKRGDVKVIV 201
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RESULT 15
US-09-934-289A-42
; Sequence 42, Application US/09934289A
; Patent No. 6852837
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MEIO98-061C1CNI(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 03/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(38)
US-09-934-289A-42

```

```

Query Match      12.9%; Score 71; DB 2; Length 277;
Best Local Similarity 35.9%; Pred. No. 1.6;
Matches 14; Conservative 10; Mismatches 11; Indels 4; Gaps 2;

Qy      41 MWVF--SIALMFVCLIMMLICLKERRARPPYRPII 76
Db      202 VMWFLSGSLVIVVCSTV-GLIICVKRRKRGDVVKVIV 239

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Search completed: January 18, 2006, 19:48:54
Job time : 23 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	551	100.0	101	3	US-09-392-822-9	Sequence 9, Appli
2	551	100.0	101	3	US-09-814-292-4	Sequence 4, Appli
3	551	100.0	101	3	US-09-875-228-5	Sequence 5, Appli
4	551	100.0	101	3	US-09-898-883-23	Sequence 23, Appl
5	551	100.0	101	3	US-09-151-376-11	Sequence 11, Appl
6	551	100.0	101	3	US-09-814-357-18	Sequence 18, Appl
7	551	100.0	101	3	US-09-814-351-18	Sequence 18, Appl
8	551	100.0	101	4	US-10-045-116-20	Sequence 20, Appl
9	551	100.0	101	4	US-10-222-479-22	Sequence 22, Appl
10	551	100.0	101	4	US-10-139-089-11	Sequence 11, Appl
11	551	100.0	101	4	US-10-691-045-18	Sequence 18, Appl
12	551	100.0	101	5	US-10-822-873-11	Sequence 11, Appl
13	522	94.7	95	5	US-10-938-227-8	Sequence 8, Appli
14	74	13.4	522	5	US-10-608-538-33	Sequence 33, Appl
15	72	13.1	354	4	US-10-425-115-271104	Sequence 271104,
16	71	12.9	239	3	US-09-934-289A-44	Sequence 44, Appl
17	71	12.9	239	5	US-10-932-991-44	Sequence 44, Appl
18	71	12.9	245	6	US-11-021-951-191	Sequence 191, App
19	71	12.9	277	3	US-09-934-289A-42	Sequence 42, Appl
20	71	12.9	277	4	US-10-369-300-10	Sequence 10, Appl
21	71	12.9	277	5	US-10-932-991-42	Sequence 42, Appl
22	71	12.9	283	3	US-09-924-231-2	Sequence 2, Appli
23	71	12.9	283	3	US-09-934-289A-13	Sequence 13, Appl
24	71	12.9	283	3	US-09-935-727-31	Sequence 31, Appl
25	71	12.9	283	4	US-10-020-787-2	Sequence 2, Appli
26	71	12.9	283	4	US-10-066-209-2	Sequence 2, Appli
27	71	12.9	283	4	US-10-369-300-2	Sequence 2, Appli


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; ORGANISM: Homo sapiens
US-09-151-376-11

Query Match      100.0%; Score 551; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60

QY 61 CLKRRRARPPYRPIIIVLNPHEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPYRPIIIVLNPHEKIHRLDGLKPCSLLLQYD 101

RESULT 6
US-09-814-357-18
; Sequence 18, Application US/09814357
; Publication No. US20030068307A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Chen, Yu
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION
; FILE REFERENCE: 348022001600
; CURRENT APPLICATION NUMBER: US/09/814,357
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence for ADP
US-09-814-357-18

Query Match      100.0%; Score 551; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60

QY 61 CLKRRRARPPYRPIIIVLNPHEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPYRPIIIVLNPHEKIHRLDGLKPCSLLLQYD 101

RESULT 7
US-09-814-351-18
; Sequence 18, Application US/09814351
; Publication No. US20030148520A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
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; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence for ADP
US-09-814-351-18

Query Match      100.0%; Score 551; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60

QY 61 CLKRRRARPPYRPIIIVLNPHEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPYRPIIIVLNPHEKIHRLDGLKPCSLLLQYD 101

RESULT 8
US-10-045-116-20
; Sequence 20, Application US/10045116
; Publication No. US20030026792A1
; GENERAL INFORMATION:
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; TITLE OF INVENTION: EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,116
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-045-116-20

Query Match      100.0%; Score 551; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
```

Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHLRDLGLKPCSLLLQYD 101
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHLRDLGLKPCSLLLQYD 101

RESULT 9
US-10-222-479-22
; Sequence 22, Application US/10222479
; Publication No. US20030091538A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS
; OF USE
; THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/222,479
; FILING DATE: 16-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/614,495
; FILING DATE: 11-Jul-2000
; APPLICATION NUMBER: 09/033,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-222-479-22

Query Match 100.0%; Score 551; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60

Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHLRDLGLKPCSLLLQYD 101
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHLRDLGLKPCSLLLQYD 101

RESULT 11
US-10-691-045-18
; Sequence 18, Application US/10691045
; Publication No. US20040146489A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/10/691,045
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: US/09/814,351
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18

RESULT 10
US-10-139-089-11
; Sequence 11, Application US/10139089
; Publication No. US20030152553A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/10/139,089
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; PRIOR APPLICATION NUMBER: 09/509,591
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/033,428
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,597
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,333
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,762
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-089-11

Query Match 100.0%; Score 551; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60

Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHLRDLGLKPCSLLLQYD 101
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHLRDLGLKPCSLLLQYD 101

RESULT 11
US-10-691-045-18
; Sequence 18, Application US/10691045
; Publication No. US20040146489A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/10/691,045
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: US/09/814,351
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18


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; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence for ADP
US-10-691-045-18

Query Match      100.0%; Score 551; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTAPTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTAPTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60

QY 61 CLKRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101

RESULT 12
US-10-822-873-11
; Sequence 11, Application US/10822873
; Publication No. US20040241857A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-873-11

Query Match      100.0%; Score 551; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTAPTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTAPTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60

QY 61 CLKRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101

RESULT 13
US-10-938-227-8
; Sequence 8, Application US/10938227
; Publication No. US20050169890A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: Adenovirus Vectors Containing Cell
; FILE REFERENCE: Status-Specific Response Elements and Methods of Use Thereof
; FILE REFERENCE: CELL-014; 122.1
; CURRENT APPLICATION NUMBER: US/10/938,227
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/099,791
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/392,822
; PRIOR FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Adenovirus
US-10-938-227-8

Query Match      94.7%; Score 522; DB 5; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.7e-52;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 APTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLICLKRRR 66
Db 1 APTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLICLKRRR 60

QY 67 ARPPIYRPIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 ARPPIYRPIIVLNPNEKIHRLDGLKPCSLLOYD 95

RESULT 14
US-10-608-538-33
; Sequence 33, Application US/10608538
; Publication No. US20050064389A1
; GENERAL INFORMATION:
; APPLICANT: TORDO, NOEL
; APPLICANT: FERRIN, PIERRE
; APPLICANT: JACOB, YVES
; APPLICANT: BAHLOUL, CHOKRI
; TITLE OF INVENTION: CHIMERIC LYSSAVIRUS NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 03495-0188-00000
; CURRENT APPLICATION NUMBER: US/10/608,538
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US/09/549,519
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,501
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Lyssavirus sp.
; FEATURE:
; OTHER INFORMATION: Laglinga
US-10-608-538-33

Query Match      13.4%; Score 74; DB 5; Length 522;
Best Local Similarity 35.0%; Pred. No. 8.7;
Matches 21; Conservative 8; Mismatches 19; Indels 12; Gaps 3;

QY 24 LNLQVHAFVNDWASLDMMWFSIALM-----FVCLIIIMWLICLKRRRRAPPIYRP 74
Db 437 VHMPPDVHKLVD---VDLGLPDWSLYALIGATIIAIFILICIRICKKRRRNSPTNRP 493

RESULT 15
US-10-425-115-271104
; Sequence 271104, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 271104
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_178843C.1.pep
US-10-425-115-271104

Query Match      13.1%; Score 72; DB 4; Length 354;
Best Local Similarity 26.0%; Pred. No. 9.8;
Matches 27; Conservative 11; Mismatches 34; Indels 32; Gaps 4;

Qy      3 GSTIAPTDDYRNTT-----ATGLTSALNLPQVHAFVNDWASLDMMWFSTALMFVCLIM 56
Db      90 GGTAPPEPNSYTVFHVIGDIVALLDALHLPQVFGVGHWDGA-----IVS 134

Qy      57 WLICLKRREARPEIYRPIIVLNPHNEKIHRLDGLKPCSLLLQY 100
Db      135 WNLCLLRPDRV-----ALVNLSVAFMPRRPGVKP----LEY 167
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Search completed: January 19, 2006, 19:50:07
Job time : 62 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:46:37 ; Search time 9 Seconds
(without alignments)
113.725 Million cell updates/sec

Title: US-10-822-873-11
Perfect score: 551
Sequence: 1 WTGSTIAPTDTYNTATGL.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA_New.*
- 1: /cgn2_6/prodata1/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/prodata1/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata1/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata1/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/prodata1/pubpaa/US09_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata1/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata1/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	12.9	283	6	US-10-987-663-4
2	62.5	11.3	222	7	US-11-212-443-174
3	59.5	10.8	222	7	US-11-212-443-175
4	57.5	10.4	1196	6	US-10-613-744-9
5	57	10.3	232	6	US-10-821-234-1199
6	57	10.3	273	6	US-10-353-783-50
7	56	10.2	85	6	US-10-966-648-6
8	56	10.2	103	6	US-10-966-648-27
9	56	10.2	112	6	US-10-966-648-2
10	56	10.2	1191	7	US-11-139-435-2
11	56	10.2	1274	6	US-10-454-437-360
12	55	10.0	113	6	US-10-467-657-5542
13	55	10.0	274	6	US-10-353-783-51
14	55	10.0	593	7	US-11-212-443-64
15	55	10.0	3716	7	US-11-052-554A-141
16	54.5	9.9	269	7	US-11-055-822-510
17	54	9.8	389	6	US-10-467-657-4468
18	54	9.8	717	6	US-10-467-657-8056
19	54	9.8	739	7	US-11-082-389-94
20	54	9.8	772	7	US-11-147-238-2
21	54	9.8	772	7	US-11-147-238-5
22	54	9.8	1150	7	US-11-139-435-1
23	54	9.8	1193	7	US-11-139-435-3
24	53.5	9.7	225	6	US-10-467-657-2276
25	53.5	9.7	468	6	US-10-957-569-28

26	53	9.6	178	6	US-10-521-162-7	Sequence 7, Appli
27	53	9.6	226	7	US-11-148-012-3	Sequence 3, Appli
28	53	9.6	309	7	US-11-165-160-2	Sequence 2, Appli
29	53	9.6	386	7	US-11-055-822-586	Sequence 586, App
30	53	9.6	650	6	US-10-467-657-1948	Sequence 1948, Ap
31	52.5	9.5	226	7	US-11-148-012-2	Sequence 2, Appli
32	52.5	9.5	366	6	US-10-661-426-4	Sequence 4, Appli
33	52.5	9.5	366	6	US-10-661-426-7	Sequence 7, Appli
34	52.5	9.5	366	6	US-10-661-426-13	Sequence 13, Appli
35	52.5	9.5	1304	6	US-10-821-234-1648	Sequence 1648, Ap
36	52	9.4	64	7	US-11-000-463-259	Sequence 259, App
37	52	9.4	187	5	US-09-978-360A-758	Sequence 758, App
38	52	9.4	598	7	US-11-113-837-18	Sequence 18, Appli
39	51.5	9.3	266	6	US-10-353-783-57	Sequence 57, Appli
40	51.5	9.3	557	7	US-11-191-374-4	Sequence 4, Appli
41	51.5	9.3	557	7	US-11-191-375-4	Sequence 4, Appli
42	51.5	9.3	557	7	US-11-191-588-4	Sequence 4, Appli
43	51.5	9.3	801	6	US-10-454-437-278	Sequence 278, App
44	51.5	9.3	801	7	US-11-174-150-29	Sequence 29, Appli
45	51.5	9.3	801	7	US-11-124-368A-292	Sequence 292, Appli

ALIGNMENTS

RESULT 1
US-10-987-663-4
; Sequence 4, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; FILE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-4

Query Match 12.9%; Score 71; DB 6; Length 283;
Best Local Similarity 35.9%; Pred. No. 0.17;
Matches 14; Conservative 10; Mismatches 11; Indels 4; Gaps 2;
QY 41 MWVF---STALMFVCLIIIMWLICLKRRRRRPPPIVPII 76
DB 202 VMWFLGSLVIVIVCVSTV-GLIICVKRKRPRGVDVKVIV 239

RESULT 2
US-11-212-443-174
; Sequence 174, Application US/11212443
; Publication No. US20050287165A1
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens

```
/ FILE REFERENCE: CHIR0159
/ CURRENT APPLICATION NUMBER: US/11/212,443
/ CURRENT FILING DATE: 2005-08-24
/ PRIOR APPLICATION NUMBER: US/09/302,626
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: PCT/IB99/00103
/ PRIOR FILING DATE: 1999-01-14
/ NUMBER OF SEQ ID NOS: 195
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 174
/ LENGTH: 222
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: ORF39
/
/ NAME/KEY: SITE
/ LOCATION: (17)..(33)
/ OTHER INFORMATION: place-holder
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (53)..(67)
/ OTHER INFORMATION: place-holder
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (211)
/ OTHER INFORMATION: place-holder
/
/ US-11-212-443-174

Query Match 11.3%, Score 62.5, DB 7, Length 222;
Best Local Similarity 25.2%, Pred. No. 1.4;
Matches 26; Conservative 15; Mismatches 37; Indels 25; Gaps 5;

Qy 3 GSTIAPTD---VRN-TTATGLTSALNLPQVHAFVNDWASLDNMWFSIALMFVCLIMWL 58
Db 113 GDTVARVEIQIRNFLTQALTSVLDLAFSFIFL-----AVMWYTSSTLTWVVLASLIC 167

Qy 59 ICCLKRRRARPPIVRPIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
Db 168 ICA-----NRTVLII-----AHRUSTVKTARIITAMD 194

RESULT 3
US-11-212-443-175
/ Sequence 175, Application US/11212443
/ Publication No. US20050287165A1
/ GENERAL INFORMATION:
/ APPLICANT: Scalato, Enzo
/ APPLICANT: Massignani, Vega
/ APPLICANT: Rappuoli, Rino
/ APPLICANT: Pizza, Mariagrazia
/ APPLICANT: Grandi, Guido
/ TITLE OF INVENTION: Meningococcal Antigens
/ FILE REFERENCE: CHIR0159
/ CURRENT APPLICATION NUMBER: US/11/212,443
/ CURRENT FILING DATE: 2005-08-24
/ PRIOR APPLICATION NUMBER: US/09/302,626
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: PCT/IB99/00103
/ PRIOR FILING DATE: 1999-01-14
/ NUMBER OF SEQ ID NOS: 195
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 175
/ LENGTH: 222
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: overlap identity
/
/ NAME/KEY: SITE
/ LOCATION: (16)..(33)
/ OTHER INFORMATION: absent or positive
/ FEATURE:
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; LOCATION: (192)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (197)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (199)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (201)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (203)..(204)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (209)..(212)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (214)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (219)..(220)
; OTHER INFORMATION: absent or positive
US-11-212-443-175

Query Match      10.8%; Score 59.5; DB 7; Length 222;
Best Local Similarity 25.2%; Pred. No. 3.3;
Matches 26; Conservative 13; Mismatches 39; Indels 25; Gaps 5;

QY      3 GSTIAPTD--YRN-TTATGTSALNLPQVHAFVNDWASLDMWFSLMFVCLIIIMWL 58
DB      113 GDTVARVELXOIRNLTGQAULTXLDLFSPF-----XAVMYYSXXLTXXVLXLXC 167
QY      59 ICCLKRRRAPPPIYPPIIVLNPHNEKIHRLDGLKPCSLLOYD 101
DB      168 IC-----XNRVLII-----AHLSTVKKAXEILXMD 194

RESULT 4
US-10-613-744-9
; Sequence 9, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-0029010S
; CURRENT APPLICATION NUMBER: US/10/613,744
; PRIOR FILING DATE: 2003-07-03
; PRIOR FILING DATE: 1999-03-24
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-04-02
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

Query Match      10.3%; Score 57; DB 6; Length 232;
Best Local Similarity 21.6%; Pred. No. 6.9;
Matches 21; Conservative 15; Mismatches 27; Indels 34; Gaps 4;

QY      31 AFVNDWASLDMW-----WFSIAL-----MFVCLIIIMWL---CCLKRR 65
DB      64 AFENNEKTKEFWSTYTAKAQGESNGSDWFOFYTFPLIFGLFIILLVFLIWRCFLUNK 123
QY      66 RARP-----PIYRPIIVLNPHNEKIHRLDGLKP 93
DB      124 TRRQTVEGHIPFPQHLLNIITPPPPPDEVDSSGLSP 160

RESULT 6
US-10-353-783-50
; Sequence 50, Application US/10353783
; Publication No. US20050261175A1
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Bosselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/353,783
/ FILING DATE: 28-Jan-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/448,729
/ FILING DATE: 24-MAY-1995
/ APPLICATION NUMBER: 08/172,329
/ FILING DATE: 21-DEC-1993
/ APPLICATION NUMBER: 07/982,255
/ FILING DATE: 25-NOV-1992
/ APPLICATION NUMBER: 07/684,535
/ FILING DATE: 10-APR-1991
/ APPLICATION NUMBER: 07/589,701
/ FILING DATE: 01-OCT-1990
/ APPLICATION NUMBER: 07/573,616
/ FILING DATE: 24-AUG-1990
/ APPLICATION NUMBER: 07/537,198
/ FILING DATE: 11-JUN-1990
/ APPLICATION NUMBER: 07/422,383
/ FILING DATE: 16-OCT-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clough, David W.
/ REGISTRATION NUMBER: 36,107
/ REFERENCE/DOCKET NUMBER: 01017/32958A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312/474-6300
/ TELEFAX: 312/474-0448
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 50:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 273 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-353-783-50

Query Match 10.3%; Score 57; DB 6; Length 273;
Best Local Similarity 26.0%; Pred. No. 8.3; Indels 20; Gaps 5;
Matches 27; Conservative 18; Mismatches 39;

QY 1 MTGSTIAPTDTYRNTTATGLTSALNLPQVHA--FVNDWASLD-----MMWFSLA 47
Db 164 VVSSTLSPEKDSR-----VSVTKPFLPPVAASSLRNDSSSNRKAKNPTGDSLSLHWAAMA 219

QY 48 L-MPVCLIIIMWLICCLKRRRARRPIYRPI--IVLNPHNEKHRL 89
Db 220 LPAPFSLIIGFAFGALYWKRPQSLTRAveniQINEEDNEISML 263

RESULT 7
US-10-966-648-6
/ Sequence 6, Application US/10966648
/ Publication No. US20050249734A1
/ GENERAL INFORMATION:
/ APPLICANT: Sutcliffe, J. Gregor
/ APPLICANT: de Lecea, Luis
/ APPLICANT: Henriksen, Steven J.
/ APPLICANT: Siggins, George R.
/ TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
/ FILE REFERENCE: 14740A-000640US
/ CURRENT APPLICATION NUMBER: US/10/966,648
/ FILING DATE: 2004-10-14
/ PRIOR APPLICATION NUMBER: US 08/648,322
/ PRIOR FILING DATE: 1996-05-15
/ PRIOR APPLICATION NUMBER: US 08/857,389
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR APPLICATION NUMBER: US 09/766,396
/ FILING DATE: 2001-01-18
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Rattus sp.
/ FEATURE:
/ OTHER INFORMATION: positions 10-112 of rat prepro cortistatin (CST),
/ OTHER INFORMATION: cortistatin-29
US-10-966-648-27

Query Match 10.2%; Score 56; DB 6; Length 103;
Best Local Similarity 36.4%; Pred. No. 3.8;
Matches 12; Conservative 5; Mismatches 4; Indels 12; Gaps 2;

QY 62 LKRRRARRPIYRPIIVLNPHNEKHRLDGLKPC 94
Db 71 LSKRQRRPPLQOP-----PHRDK-----KPC 91

RESULT 9
US-10-966-648-2
/ Sequence 2, Application US/10966648
/ Publication No. US20050249734A1
/ GENERAL INFORMATION:
/ APPLICANT: Sutcliffe, J. Gregor
/ APPLICANT: de Lecea, Luis
/ APPLICANT: Henriksen, Steven J.
/ APPLICANT: Siggins, George R.
/ TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
/ FILE REFERENCE: 14740A-000640US
/ CURRENT APPLICATION NUMBER: US/10/966,648
/ FILING DATE: 2004-10-14
/ PRIOR APPLICATION NUMBER: US 08/648,322
/ PRIOR FILING DATE: 1996-05-15
/ PRIOR APPLICATION NUMBER: US 08/857,389
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR APPLICATION NUMBER: US 09/766,396
/ FILING DATE: 2001-01-18
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Rattus sp.
/ FEATURE:
/ OTHER INFORMATION: positions 10-112 of rat prepro cortistatin (CST),
/ OTHER INFORMATION: cortistatin-29
US-10-966-648-27

Query Match 10.2%; Score 56; DB 6; Length 85;
Best Local Similarity 36.4%; Pred. No. 3;
Matches 12; Conservative 5; Mismatches 4; Indels 12; Gaps 2;

QY 62 LKRRRARRPIYRPIIVLNPHNEKHRLDGLKPC 94
Db 53 LSKRQRRPPLQOP-----PHRDK-----KPC 73

RESULT 8
US-10-966-648-27
/ Sequence 27, Application US/10966648
/ Publication No. US20050249734A1
/ GENERAL INFORMATION:
/ APPLICANT: Sutcliffe, J. Gregor
/ APPLICANT: de Lecea, Luis
/ APPLICANT: Henriksen, Steven J.
/ APPLICANT: Siggins, George R.
/ APPLICANT: The Scripps Research Institute
/ TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
/ FILE REFERENCE: 14740A-000640US
/ CURRENT APPLICATION NUMBER: US/10/966,648
/ FILING DATE: 2004-10-14
/ PRIOR APPLICATION NUMBER: US 08/648,322
/ PRIOR FILING DATE: 1996-05-15
/ PRIOR APPLICATION NUMBER: US 08/857,389
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR APPLICATION NUMBER: US 09/766,396
/ FILING DATE: 2001-01-18
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Rattus sp.
/ FEATURE:
/ OTHER INFORMATION: positions 10-112 of rat prepro cortistatin (CST),
/ OTHER INFORMATION: cortistatin-29
US-10-966-648-27

Query Match 10.2%; Score 56; DB 6; Length 85;
Best Local Similarity 36.4%; Pred. No. 3;
Matches 12; Conservative 5; Mismatches 4; Indels 12; Gaps 2;

QY 62 LKRRRARRPIYRPIIVLNPHNEKHRLDGLKPC 94
Db 53 LSKRQRRPPLQOP-----PHRDK-----KPC 73

RESULT 8
US-10-966-648-27
/ Sequence 27, Application US/10966648
/ Publication No. US20050249734A1
/ GENERAL INFORMATION:
/ APPLICANT: Sutcliffe, J. Gregor
/ APPLICANT: de Lecea, Luis
/ APPLICANT: Henriksen, Steven J.
/ APPLICANT: Siggins, George R.
/ APPLICANT: The Scripps Research Institute
/ TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
/ FILE REFERENCE: 14740A-000640US
/ CURRENT APPLICATION NUMBER: US/10/966,648
/ FILING DATE: 2004-10-14
/ PRIOR APPLICATION NUMBER: US 08/648,322
/ PRIOR FILING DATE: 1996-05-15
/ PRIOR APPLICATION NUMBER: US 08/857,389
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR APPLICATION NUMBER: US 09/766,396
/ FILING DATE: 2001-01-18
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Rattus sp.
/ FEATURE:
/ OTHER INFORMATION: positions 10-112 of rat prepro cortistatin (CST),
/ OTHER INFORMATION: cortistatin-29
US-10-966-648-27

Query Match 10.2%; Score 56; DB 6; Length 103;
Best Local Similarity 36.4%; Pred. No. 3.8;
Matches 12; Conservative 5; Mismatches 4; Indels 12; Gaps 2;

QY 62 LKRRRARRPIYRPIIVLNPHNEKHRLDGLKPC 94
Db 71 LSKRQRRPPLQOP-----PHRDK-----KPC 91

RESULT 9
US-10-966-648-2
/ Sequence 2, Application US/10966648
/ Publication No. US20050249734A1
/ GENERAL INFORMATION:
/ APPLICANT: Sutcliffe, J. Gregor
/ APPLICANT: de Lecea, Luis
/ APPLICANT: Henriksen, Steven J.
/ APPLICANT: Siggins, George R.
/ TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods
/ FILE REFERENCE: 14740A-000640US
/ CURRENT APPLICATION NUMBER: US/10/966,648
/ FILING DATE: 2004-10-14
/ PRIOR APPLICATION NUMBER: US 08/648,322
/ PRIOR FILING DATE: 1996-05-15
/ PRIOR APPLICATION NUMBER: US 08/857,389
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR APPLICATION NUMBER: US 09/766,396
/ FILING DATE: 2001-01-18
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 27
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Rattus sp.
/ FEATURE:
/ OTHER INFORMATION: positions 10-112 of rat prepro cortistatin (CST),
/ OTHER INFORMATION: cortistatin-29
US-10-966-648-27
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; FILE REFERENCE: 1470A-000640US
; CURRENT APPLICATION NUMBER: US/10/966,648
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 08/648,322
; PRIOR FILING DATE: 1996-05-15
; PRIOR APPLICATION NUMBER: US 08/857,389
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: US 09/766,396
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat preprocortistatin
; NAME/KEY: SIGNAL
; LOCATION: (1)..(27)
; OTHER INFORMATION: signal peptide
US-10-966-648-2

Query Match 10.2%; Score 56; DB 6; Length 112;
Best Local Similarity 36.4%; Pred. No. 4.1;
Matches 12; Conservative 5; Mismatches 4; Indels 12; Gaps 2;

Qy 62 LKRRARPPIYRIIVLNPNHKEIHRDLGKPC 94
| : : : : : : : : : : : : : : : : : :
Db 80 LSKRQRPPLQKP-----PDRK-----KPC 100

RESULT 10
US-11-139-435-2
; Sequence 2, Application US/11139435
; Publication No. US20050287664A1
; GENERAL INFORMATION:
; APPLICANT: Fann, Ming-Ji
; TITLE OF INVENTION: Cellular Proliferation Control Factors
; FILE REFERENCE: 17741-002001
; CURRENT APPLICATION NUMBER: US/11/139,435
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,611
; PRIOR FILING DATE: 2004-05-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1191
; TYPE: PRT
; ORGANISM: M. musculus
US-11-139-435-2

Query Match 10.2%; Score 56; DB 7; Length 1191;
Best Local Similarity 30.4%; Pred. No. 55;
Matches 17; Conservative 9; Mismatches 20; Indels 10; Gaps 2;

Qy 53 LIIMWLIICLKRARRPPIYRIIVLNPNH-----KTHR---LDGLKPCSLLL 98
: : : : : : : : : : : : : : : : : :
Db 527 LIIVSWLPPIAKYRRGQVLYRLSFRLLSTENAIQVELPQTVHEYLLEGLKPDVYL 582

RESULT 11
US-10-454-437-360
; Sequence 360, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habethauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 360
; LENGTH: 1274
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-360

Query Match 10.2%; Score 56; DB 6; Length 1274;
Best Local Similarity 20.2%; Pred. No. 59;
Matches 18; Conservative 21; Mismatches 28; Indels 22; Gaps 5

Qy 2 TGSTTAPTDTYRNTATGLTSALNLPQVHAFVNDWASLDMM--WF-----SIALMF 50
| : : : : : : : : : : : : : : : : : :
Db 1060 TARRLLAPIT-----SGVLAALSLLMQYLLTEF---NMWITWLLGGLILMTVGLVANG 1105

Qy 51 VCLIIIMWLIICLKRARRPPIYRIIVLN 79
| : : : : : : : : : : : : : : : : : :
Db 1110 ITVVMKW-VCVGKHKPSEHPFSLFRFWLN 1137

RESULT 12
US-10-467-657-5542
; Sequence 5542, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5542
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5542

Query Match 10.0%; Score 55; DB 6; Length 113;
Best Local Similarity 27.5%; Pred. No. 5.5;
Matches 11; Conservative 8; Mismatches 15; Indels 6; Gaps 2;

Qy 29 VHAFVNDWASL--DMWV-----FSIALMFVCLIMWLICCL 62

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Db 65 IAVFLHAWVGIRDLMWDYIKPFGVRLEQLQVATIVLWGCL 104

RESULT 13

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US-10-353-783-51
; Sequence 51, Application US/10353783
; Publication No. US20050261175A1
; GENERAL INFORMATION:
; APPLICANT: Zsebo, Krisztina M.
;           Bosseلمان, Robert A.
;           Suggs, Sidney V.
;           Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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Query Match      10.0%; Score 55; DB 6; Length 274;
Best Local Similarity 25.0%; Pred. No. 15;
Matches 26; Conservative 19; Mismatches 39; Indels 20; Gaps 5;

QY 1 MTGSTATTPTDYRNTTATGTTSAINTPQVHA---FVNDWAS-----LDMWFSIA 47
Db 165 VVSESTLSPDKDSR-----VSVTKPMLPPVAASISLRNDSSSSNRKASISGDSNLOWAAMA 220

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QY 48 L-MFVCLIIIMWLICLKRRAAPPPIVRPI--IVLNPHNEKIHL 88
DB 221 LPAAFFSLVTFGFAGALYWKKKOPNLTTRTVENIOINBEDNEISWL 264

RESULT 14

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US-11-212-443-64
; Sequence 64, Application US/11212443
; Publication No. US20050287165A1
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizzi, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIR0159
; CURRENT APPLICATION NUMBER: US/11/212,443
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/09/302,626
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (64)..(65)
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (134)
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (232)
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (287)
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: unknown
US-11-212-443-64

```

```

Query Match      10.0%; Score 55; DB 7; Length 593;
Best Local Similarity 32.7%; Pred. No. 34;
Matches 18; Conservative 4; Mismatches 11; Indels 22; Gaps 2;

QY  2  TGSTIAP-----TTDYRNT-TATGLTSALNLPQVHAFFVN  34
      |||||:
Db   117  TGSIVSSPEGRNTVTAKIDVEEFANNRYATDYAHTOEKGLTVALNVPVQAQGN  171

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RESULT 15

RESUMI 13
US-11-052-354A-141
; Sequence 141. Application US/11052354A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD
; TITLE OF INVENTION: PROTEINS OF THERM


```

; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141
; LENGTH: 3716
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-141

```

```

Query Match      10.0%; Score 55; DB 7; Length 3716;
Best Local Similarity 35.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 5; Mismatches 19; Indels 2; Gaps 1;
QY      6 IAPTTDYRNTTATGLTSALN--LPQVHAFVNDWASLDMWW 43
Db      2445 VPPTPGFGNTTATPSSGFFNSGAGVSGFGNGVNLGWW 2484

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Search completed: January 18, 2006, 19:50:27
Job time : 9 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:42:41 ; Search time 70 Seconds
(without alignments)
1017.977 Million cell updates/sec

Title: US-10-822-873-11
Perfect score: 551
Sequence: 1 MTGSTIAPTDTYRNTATG.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	551	100.0	101	1	E311_ADE02	P24935 human adeno
2	551	100.0	101	2	Q779E8_ADE02	Q779E8 human adeno
3	548	99.5	101	2	Q910Z3_ADE02	Q910Z3 human adeno
4	545	98.9	101	2	Q912J6_ADE02	Q912J6 human adeno
5	538	97.6	101	1	E311_ADE06	O55653 human adeno
6	355	64.4	94	2	O123J2_ADE01	O123J2 human adeno
7	346	62.8	93	1	E311_ADE05	P17590 human adeno
8	346	62.8	93	2	Q6VGT8_ADE08	Q6VGT8 human adeno
9	107.5	19.5	276	2	Q76C86_ADE08	Q76C86 human adeno
10	107.5	19.5	276	2	Q80IV7_ADE08	Q80IV7 human adeno
11	102.5	18.6	296	2	O5TIZ2_ADE09	O5TIZ2 human adeno
12	101	18.3	261	2	Q76L5_ADE08	Q76L5 human adeno
13	100.5	18.2	281	2	Q4KS19_ADE08	Q4KS19 human adeno
14	90.5	16.4	259	2	Q7TBG9_ADE08	Q7TBG9 human adeno
15	77	14.0	235	2	Q90770_CHICK	Q90770 gallus gall
16	77	14.0	235	2	Q6R133_CHICK	Q6R133 gallus gall
17	77	14.0	235	2	Q6Q65_CHICK	Q6Q65 gallus gall
18	77	14.0	235	2	Q6QR63_CHICK	Q6QR63 gallus gall
19	76.5	13.9	435	2	Q4PET9_USTWA	Q4PET9 ustulago ma
20	76.5	13.9	866	2	Q6C1Q7_KLULA	Q6C1Q7 klyveromyc
21	76	13.8	235	2	Q6QR62_CHICK	Q6QR62 gallus gall
22	76	13.8	235	2	Q6QR64_CHICK	Q6QR64 gallus gall
23	75.5	13.7	503	2	Q84Q68_ORYSA	Q84Q68 oryza sativ
24	74.5	13.5	163	2	Q87802_SIVCZ	Q87802 chimpanzee
25	74	13.4	283	2	Q9XSZ8_CERAE	Q9XSZ8 cercopithe
26	74	13.4	522	2	Q91C27_9RAB	Q91C27 lagos bat v
27	74	13.4	544	1	ADA10_RAT	Q10743 rattus norv
28	73.5	13.3	347	2	Q88TH9_LACPL	Q88TH9 lactobacill
29	73.5	13.3	1070	2	Q5KDVO_CRYNE	Q5KDVO cryptococcu
30	72	13.1	92	2	Q5C818_SCHJA	Q5C818 schistosoma
31	72	13.1	128	2	Q5C807_SCHJA	Q5C807 schistosoma

RESULT 1
E311_ADE02
ID E311_ADE02 STANDARD; PRT; 101 AA.
AC P24935;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Early E3A 11.6 kDa glycoprotein.
OS Human adenovirus 2 (HAdV-2).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=81053687; PubMed=6253880;
RA Herisse J., Courtois G., Galibert F.;
RT "Nucleotide sequence of the EcoRI D fragment of adenovirus 2 genome.";
RL Nucleic Acids Res. 8:2173-2192(1980).
RN [2]
RP IDENTIFICATION OF PROTEIN.
RX MEDLINE=93079877; PubMed=1448922;
RA Scaria A., Tollefson A.E., Saha S.K., Wold W.S.M.;
RT "The E3-11.6K protein of adenovirus is an Asn-glycosylated integral membrane protein that localizes to the nuclear membrane.";
RL Virology 191:743-753(1992).
CC -!- SUBCELLULAR LOCATION: Integral nuclear membrane protein.
CC -!- PTM: N-glycosylated and probably also O-glycosylated.
CC -!- SIMILARITY: Belongs to the adenoviruses E3A-1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
CC EMBL: J01917; AAA92222.1; -: Genomic_DNA.
DR InterPro; IPR008652; Hum_adeno_E3A.
DR Pfam; PF05393; Hum_adeno_E3A; 1.
KW Early protein; Glycoprotein; Transmembrane.
FT TRANSMEM 41 62 Potential.
FT CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 101 AA; 11644 MW; PB89FC6E921E84B CRC64;

Query Match 100.0%; Score 551; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDTYRNTATGTSALNLPQVHFVNDWASLDMWFSIALMFVCLIIIMWLC 60
Db 1 MTGSTIAPTDTYRNTATGTSALNLPQVHFVNDWASLDMWFSIALMFVCLIIIMWLC 60

Qy 61 CLKRRRRRPPPIYRPIIVLNPHEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRRRPPPIYRPIIVLNPHEKIHRLDGLKPCSLLLQYD 101

Q723K1 homo sapien
Q37535 katharina c
Q91NUS hepatitis b
Q5UGN5 mimivirus.
Q6QPG5 simian aden
Q5XQ95 xenopus lae
Q9V274 chimpanzee
Q4FWJ1 leishmania
Q8N634 homo sapien
Q92956 homo sapien
Q6IB95 homo sapien
Q6GNB1 xenopus lae
Q6CFI5 yarrowia li
Q8JNC4 macropodid

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RESULT 2
Q779E8_ADE02
ID Q779E8_ADE02 PRELIMINARY; PRT; 101 AA.
AC Q779E8;
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE 11.6K protein.
OS Human adenovirus 2 (HAdV-2).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ear swab, Respiratory epithelium, and stool sample;
RA Borchering F., Pring-Akerblom P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293914; CAC67713.1; -; Genomic DNA.
DR EMBL; AJ293916; CAC67729.1; -; Genomic DNA.
DR EMBL; AJ293917; CAC67737.1; -; Genomic DNA.
DR EMBL; AJ293912; CAC67696.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum adeno E3A.
DR PFam; PF05393; Hum adeno E3A; 1.
SQ SEQUENCE 101 AA; 11644 MW; FB89FCC6E921E84B CRC64;

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
Db 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60

Qy 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 3
Q910Z3_ADE02
ID Q910Z3_ADE02 PRELIMINARY; PRT; 101 AA.
AC Q910Z3;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE 11.6K protein.
OS Human adenovirus 2 (HAdV-2).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liquor;
RA Borchering F., Pring-Akerblom P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293915; CAC67721.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum adeno E3A.
DR PFam; PF05393; Hum adeno E3A; 1.
SQ SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;

Query Match 99.58; Score 548; DB 2; Length 101;
Best Local Similarity 99.08; Pred. No. 2.2e-52;
Matches 100; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
Db 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60

Qy 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 4
Q912J6_ADE02
ID Q912J6_ADE02 PRELIMINARY; PRT; 101 AA.
AC Q912J6;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE 11.6K protein.
OS Human adenovirus 2 (HAdV-2).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Borchering F., Pring-Akerblom P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293913; CAC67704.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum adeno E3A.
DR PFam; PF05393; Hum adeno E3A; 1.
SQ SEQUENCE 101 AA; 11704 MW; E13857DC5891E85B CRC64;

Query Match 98.9%; Score 545; DB 2; Length 101;
Best Local Similarity 99.0%; Pred. No. 4.8e-52;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
Db 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60

Qy 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 5
E311_ADE06
ID E311_ADE06 STANDARD; PRT; 101 AA.
AC O55653;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Early E3A 11.6 kDa glycoprotein.
OS Human adenovirus 6 (HAdV-6).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10534;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Reichmann H., Schaarschmidt E., Geisler B., Hausmann J., Ortmann D.,
BAUER U., Flunker G., Seidel W.;
RT "Sequence analysis of group C human adenoviruses type 1 and 6 for five
genes of region E3.";
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral nuclear membrane protein.
CC -1- PTM: N-glycosylated and probably also O-glycosylated (by
similarity).
CC -1- SIMILARITY: Belongs to the adenoviruses E3A-1 family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL; Y16037; CAA75991.1; -; Genomic DNA.
DR InterPro; IPR008652; Hum adeno E3A.
DR PFam; PF05393; Hum adeno E3A; 1.
KW Early protein; Glycoprotein; Transmembrane.
TX TRANSMEM 41 62
FT CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 101 AA; 11613 MW; EF219000939E3B4B CRC64;
```

```
Query Match          97.6%; Score 538; DB 1; Length 101;
Best Local Similarity 98.0%; Pred. No. 2.8e-51;
Matches 99; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTGSIATPTDYRTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60
DB 1 MTGSIATPTDYRTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

QY 61 CLKRRARPPIYRPIIVLPHNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRARPPIYRPIIVLPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 6
O12392_ADR01 PRELIMINARY; PRT; 94 AA.
ID O12392;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE 11.6K protein (10.7 kDa protein).
GN Names:Adi/E3-11.6K;
OS Human adenovirus 1 (HAdV-1).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hannover /Adrian German reference center for adenoviruses;
RA Reichmann H., Schaarschmidt E., Geisler B., Hausmann J., Ortmann D.,
RA Bauer U., Flunker G., Seidel W.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Hannover /Adrian German reference center for adenoviruses;
RA Reichmann H., Schaarschmidt E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15302955; DOI=10.1099/vir.0.80118-0;
RA Lauer K.P., Llorente I., Blair E., Teto J., Krasnov V.,
RA Purkayastha A., Ditty S.E., Hadfield T.L., Buck C., Tibbetts C.,
RA Seto D.;
RT "Natural variation among human adenoviruses: genome sequence and
RT annotation of human adenovirus serotype 1.";
RL J. Gen. Virol. 85:2615-2625(2004).
DR EMBL; Y11257; CAA72127.1; -; Genomic DNA.
DR EMBL; Y11032; CAA71916.1; -; Genomic DNA.
DR EMBL; AF534906; AAQ10560.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum_adenovirus E3A; I.
DR Pfam; PF05393; Hum_adenovirus E3A; I.
SQ SEQUENCE 94 AA; 10674 MW; D1148B5AFE771862 CRC64;

Query Match          64.4%; Score 355; DB 2; Length 94;
Best Local Similarity 78.8%; Pred. No. 3.8e-31;
Matches 63; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 16 TATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLCCKRRARPPIYRPI 75
DB 10 TATGTLSTQDMPQVSTFVNWNANLGMWFSIALMFVCLIIIMWLSCLCKRRARPPIYKPI 69

QY 76 IVLPHNEKIHRLDGLKPCS 95
DB 70 IVLPHNEKIHRLDGLKPCS 89

RESULT 7
E311_ADE05 STANDARD; PRT; 93 AA.
ID E311_ADR05
AC P17590;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
```

```
DE Early E3A 10.5 kDa glycoprotein.
OS Human adenovirus 5 (HAdV-5).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28285;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85092388; PubMed=2981456;
RA Cladas C., Wold W.S.M.;
RT "DNA sequence of the early E3 transcription unit of adenovirus 5.";
RL Virology 140:28-43(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=92087470; PubMed=1727603;
RA Chroboczek J., Bieber F., Jacrot B.;
RT "The sequence of the genome of adenovirus type 5 and its comparison
RT with the genome of adenovirus type 2.";
RL Virology 186:280-285(1992).
CC -!- SUBCELLULAR LOCATION: Integral nuclear membrane protein.
CC -!- PTM: N-glycosylated and probably also O-glycosylated.
CC -!- SIMILARITY: Belongs to the adenoviruses E3A-1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M73260; -; NOT ANNOTATED_CDS; Genomic_DNA.
DR EMBL; X03002; CAA36784.1; -; Genomic_DNA.
DR PIR; A05245; ERA53.
DR InterPro; IPR008652; Hum_adenovirus E3A; I.
DR Pfam; PF05393; Hum_adenovirus E3A; I.
KW Early protein; Glycoprotein; Transmembrane.
FT TRANSMEM 34 55 Potential.
FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 93 AA; 10523 MW; 008AD087AAB45A8F CRC64;

Query Match          62.8%; Score 346; DB 1; Length 93;
Best Local Similarity 78.3%; Pred. No. 3.7e-30;
Matches 65; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 14 NTT-----ATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLCCKRRARP 69
DB 3 NTTNAAATGLTSTNTPTQVSAPVNNWNLGMWFSIALMFVCLIIIMWLCCKRRARP 62

QY 70 PIYRPIIVLPHNEKIHRLDGLK 92
DB 63 PIYRPIIVLPHNEKIHRLDGLK 85

RESULT 8
Q6VGT8_9ADEN PRELIMINARY; PRT; 93 AA.
ID Q6VGT8_9ADEN PRELIMINARY; PRT; 93 AA.
AC Q6VGT8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E3 10.5K.
OS Human adenovirus C.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=129951;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA McAllister D.L., Lu F., Thomas B.K., Hutchins B.M., Sugarman B.J.;
RT "Complete Nucleic Acid Sequence of the Adenovirus Type 5 Reference
RT Material.";
RL Bioprocessing 0:0-0(2003).
DR EMBL; AY339865; AAQ19306.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum_adenovirus E3A; I.
DR Pfam; PF05393; Hum_adenovirus E3A; I.
SQ SEQUENCE 93 AA; 10523 MW; 008AD087AAB45A8F CRC64;
```



```

Best Local Similarity   24.0%; Pred. No. 0.01;
Matches 18; Conservative 23; Mismatches 34; Indels 0; Gaps 0;

Qy      2 TGSTIAPTDTYRNTTATGLTSALNLPQHAFVNDWASLDMMWFSTIALMFVCLIIIMWLICC 61
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db      165 TDATLSAFSSANTLSTLANWTETGVLMLHGQPYSGLHIQTITFLVCIGIFILVLLYFVCC 224

Qy      62 LKRRARRPPIYPRII 76
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db      225 KARKKSRRPIYRPVI 239

RESULT 13
ID Q4KS19_9ADEN PRELIMINARY; PRT; 281 AA.
AC Q4KS19;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 281R.
OS Human adenovirus type 46.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=46941;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Police S.R.;
RT "Genome Sequence of Human adenovirus type 46.";
RL Submitted (DSC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY875648; AAX70939.1; -; Genomic DNA.
SQ SEQUENCE 281 AA; 30918 MW; 23CFB1230DA2032 CRC64;

Query Match          18.2%; Score 100.5; DB 2; Length 281;
Best Local Similarity 26.2%; Pred. No. 0.012;
Matches 21; Conservative 22; Mismatches 24; Indels 13; Gaps 3;

Qy      9 TTDYRNTTATGLTSALNLPQHAFVND-----WASLD--MWTFSTIALMFVCLIIIM 56
||:| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db      181 TTQEATSSAFSSANTLTSL-AWTNETGVSLMNRQPSGLDIQITFLVVGIGFILAVLL 239

Qy      57 WLICCLKERRARPPIYRII 76
|:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db      240 YFVCKKAREKSRRPIYRPVI 259

RESULT 14
Q7TBG9_ADE08
ID Q7TBG9_ADE08 PRELIMINARY; PRT; 259 AA.
AC Q7TBG9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E3B1.29.1k.
OS Human adenovirus 8 (HAdV-8).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=31545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H16;
RX PubMed=12560390; DOI=10.1136/jcp.56.2.120;
RA Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
RA Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukoyama A., Matsuno S.,
RA Inada T., Okabe N.;
RT Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima
RT City over a 15-year Period.;
RL J. Clin. Pathol. 56:120-125(2003).
DR EMBL; AB102672; BAC78834.1; -; Genomic DNA.
SQ SEQUENCE 259 AA; 29138 MW; D3742E9ADBAC5CF4 CRC64;

Query Match          16.4%; Score 90.5; DB 2; Length 259;
Best Local Similarity 22.5%; Pred. No. 0.14;
Matches 18; Conservative 23; Mismatches 26; Indels 13; Gaps 2;

Qy      9 TTDYRNTTATGLTSALNLPQHAFVND-----WASLDMMWFSTIALMFVCLIIIM 56

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:43:21 ; Search time 16 Seconds
(without alignments)
607.368 Million cell updates/sec

Title: US-10-822-873-11
Perfect score: 551
Sequence: 1 MTGSTAPTDRYNTATG.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	346	62.8	93	1 ERAD53	early E3A 10.5K pr
2	77	14.0	235	2 I50610	T-cell surface gly
3	74	13.4	544	2 S52477	disintegrin (EC 3
4	72	13.1	316	2 S50336	NADH2 dehydrogenas
5	70	12.7	324	2 T01316	epoxide hydrolase
6	70	12.7	748	2 S66129	disintegrin (EC 3
7	69.5	12.6	95	2 S72597	hypothetical prote
8	69.5	12.6	518	2 AG0784	rtm protein [impor
9	68	12.3	429	2 AH2409	hypothetical prote
10	67.5	12.3	340	2 T28767	hypothetical prote
11	67.5	12.3	1187	2 T19413	hypothetical prote
12	67	12.2	491	2 S52320	disintegrin (EC 3
13	67	12.2	522	2 A46103	transmembrane gly
14	67	12.2	533	2 T19416	hypothetical prote
15	66.5	12.1	428	2 T48284	hypothetical prote
16	66	12.0	244	2 T22046	hypothetical prote
17	65.5	11.9	306	2 T19412	hypothetical prote
18	65	11.8	279	2 S42125	hypothetical prote
19	65	11.8	466	2 S52258	copper resistance
20	64.5	11.7	242	2 T22922	hypothetical prote
21	64.5	11.7	871	1 I48696	protein-tyrosine k
22	64.5	11.7	881	1 I48697	protein-tyrosine k
23	64	11.6	518	1 T69804	multidrug-efflux t
24	63.5	11.5	83	2 T36483	probable membrane
25	63.5	11.5	150	2 E96521	protein F21D18.14
26	63.5	11.5	254	2 F87652	hypothetical prote
27	63.5	11.5	501	2 T14339	sucrose-proton tra
28	63.5	11.5	638	2 H82690	hypothetical prote
29	63.5	11.5	1667	2 T15863	hypothetical prote

30	63	11.4	138	1 Q08EB2	UL73 glycoprotein
31	63	11.4	389	2 S67506	large surface anti
32	63	11.4	458	2 S61974	SSu1 protein - yea
33	63	11.4	462	2 C70597	hypothetical prote
34	63	11.4	844	2 T00529	hypothetical prote
35	62.5	11.3	137	2 E88382	protein W06E11.6 l
36	62.5	11.3	332	2 T02789	probable membrane
37	62.5	11.3	558	2 E84324	TRK potassium upa
38	62	11.3	162	2 F82493	hypothetical prote
39	62	11.3	256	2 AH1148	hypothetical prote
40	62	11.3	756	2 S74742	exopolysaccharide
41	61.5	11.2	262	2 S47427	E1 membrane glycop
42	61.5	11.2	283	2 T15964	hypothetical prote
43	61.5	11.2	410	2 C36671	mating-type locus
44	61.5	11.2	410	2 D32696	b3 protein - smut
45	61.5	11.2	603	2 B86215	protein T6D22.10 l

ALIGNMENTS

RESULT 1

ERAD53
early E3A 10.5K protein - human adenovirus 5
C;Species: Mastadenovirus h5 (human adenovirus 5)
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A05245
R;Cladaras, C.; Wold, W.S.M.
Virology 140, 28-43, 1985
A;Title: DNA sequence of the early E3 transcription unit of adenovirus 5.
A;Reference number: A94335; MUID:85092388; PMID:2981456
A;Accession: A05245
A;Molecule type: DNA
A;Residues: 1-93 <CLA>
A;Cross-references: UNIPROT:P17590; UNIPARC:UPI0000037966; GB:X03002; NID:G58503; PIDN:C
C;Superfamily: adenovirus early E3A 10.5K protein
C;Keywords: early protein; transmembrane protein

Query Match 62.8%; Score 346; DB 1; Length 93;
Best Local Similarity 78.3%; Pred. No. 6.2e-31;
Matches 65; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

Qy	14	NTT-----ATGLFSALNLPQVHAFVNDWASLDMMWFSLMFVCLIMWLICCLKRRARP	69
Db	3	NTTNAAGATGLTSTTTPQVSFAFVNDNLGMWFSIALMFVCLIMWLICCLKRRARP	62
Qy	70	PYRPIIVLNPHEKIHRLDGLK	92
Db	63	PYSPPIVLPNNNGIHRLDGLK	85

RESULT 2

I50610
T-cell surface glycoprotein CD8 alpha chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50610; S33350
R;Tregaskes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison, J. Immunol. 154, 4485-4494, 1995
A;Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha a lymphocytes.
A;Reference number: I50609; MUID:95238946; PMID:7722305
A;Accession: I50610
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-235 <TR>
A;Cross-references: UNIPROT:Q90770; UNIPARC:UPI000000FBABF; EMBL:222726; NID:G488149; PIDN:C
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein

Query Match 14.0%; Score 77; DB 2; Length 235;
Best Local Similarity 25.2%; Pred. No. 0.55;


```
Matches 27; Conservative 17; Mismatches 26; Indels 44; Gaps 6;
QY 3 GSTI-----APTTDYN-----TTATG-----LTSALNLPQVHAFVNDWASLDMW 43
Db 621 GRTITLQPSPCNDFRGYCDVFMRCRLVDAGPLARLKKAIKAFSPELYENIAEW--IVAYW 678
QY 44 FSIALMFVCLIIIMWL-----IC-----CLKRRRARPPPIVRP 74
Db 679 WAVLLMGIALIIMLMAGFIKCSVHTPSSNPKLPPPKPLGTLKRRRPQPIQOP 732
RESULT 7
S72597
hypothetical protein B1937_F2.47 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S72597
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Reference number: S72580
A:Accession: S72597
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <SWI>
A:Cross-references: UNIPROT:Q49760; UNIPARC:UPI0000139B2E; EMBL:U00016; NID:G466961; PID:
Query Match 12.6%; Score 69.5; DB 2; Length 95;
Best Local Similarity 29.2%; Pred. No. 1.5;
Matches 14; Conservative 13; Mismatches 20; Indels 1; Gaps 1;
QY 9 TTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIM 56
Db 13 TVFYDAGTANG-TNGISVSPVNGFLNWDLSIELWLSGLAFVLQALVM 59
RESULT 8
AG0784
rtm protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG0784
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:111677608
A:Accession: AG0784
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-518 <PAR>
A:Cross-references: UNIPARC:UPI0000059BBE; GB:AL513382; PIDN:CAD02597.1; PID:G16503453;
C:Genetics:
A:Gene: rtm
C:Superfamily: probable membrane protein ylaB
Query Match 12.6%; Score 69.5; DB 2; Length 518;
Best Local Similarity 26.4%; Pred. No. 8.1;
Matches 24; Conservative 13; Mismatches 27; Indels 27; Gaps 6;
QY 5 TTA--PTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCL--IIMWLIC 60
Db 203 TVAELPGTSPQATNGLPKIQI-----YADSWTYNDLWY---ALMLGICISIVAGFIC 254
QY 61 -CLKRRRARP-----PIYRPII 76
Db 255 YFIYALRTRPGKEILLTAIKHEQFYVYQPV 285
RESULT 9
AH2409
```

```
hypothetical protein all4832 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AH2409
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A>Title: Complete genomic sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2409
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-429 <KUR>
A:Cross-references: UNIPROT:O8YM05; UNIPARC:UPI00000CEC7A; GB:BA000019; PIDN:BAB76531.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4832
Query Match 12.3%; Score 68; DB 2; Length 429;
Best Local Similarity 21.2%; Pred. No. 9.8;
Matches 24; Conservative 19; Mismatches 36; Indels 34; Gaps 4;
QY 1 WTGSTIAPT-----TDYRN-----TTATGTSALNLPQVH----- 30
Db 128 LFGATLAPDPLVASEVQLTDINDKDELRFGLTSEGLNDALAFPPFVYFGLFAIKDDNMN 187
QY 31 AFVNDWASLDMWFSIALMF-----VCLIIIMWLICLKRRRARPPPIYRPIIVLN 79
Db 188 TWFQKQVAVDLIWAATALINGFVVAKAIVIDQVKQKRSADALMEDFIALS 240
RESULT 10
T28767
hypothetical protein W03D2.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28767
R:Rohlfing, T.; Wohlmann, P.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of C. elegans cosmid W03D2.
A:Reference number: Z20519
A:Accession: T28767
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <ROH>
A:Cross-references: UNIPROT:O45217; UNIPARC:UPI000007BBD5; EMBL:AF000298; PIDN:AAC48262.1
A:Experimental source: strain Bristol N2; clone W03D2
C:Genetics:
A:Gene: CESP:W03D2.10
A:Map position: 4
A:Introns: 63/3; 118/2; 185/3; 210/3; 253/3; 314/1
Query Match 12.3%; Score 67.5; DB 2; Length 340;
Best Local Similarity 25.0%; Pred. No. 8.7;
Matches 21; Conservative 16; Mismatches 30; Indels 17; Gaps 4;
QY 19 GLTSALNLPQ-----VHAFVNDWASLDMWFS-IALMFVCLIIIMWLICLKRRRAR 68
Db 53 GLVEVLTLPERVIVHAGSIVLFDVSFLYEKVIANPLAALYACSPALCITLL-----AS 107
QY 69 PPIYRPIIVLNPHNPKIHRLDGLK 92
Db 108 HFVFRYIAVCRPHD--LHHLEGWK 129
RESULT 11
T19413
hypothetical protein C23H4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19413
R:Wilkinson, J.
```

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19121
A:Accession: T19413
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1187 <WIL>
A:Cross-references: UNIPROT:Q93254; UNIPARC:UPI000017B7AA; EMBL:Z78416; PIDN:CAB01680.1;
A:Experimental source: clone C23H4
C:Genetics:
A:Gene: CESP:C23H4.3
A:Map position: X
A:Introns: 48/3; 81/2; 114/3; 182/1; 278/3; 346/3; 401/1; 486/1; 538/3; 635/3; 668/2; 70

Query Match 12.3%; Score 67.5; DB 2; Length 1187;
Best Local Similarity 22.4%; Pred. No. 31;
Matches 19; Conservative 15; Mismatches 34; Indels 17; Gaps 3;

QY 4 STIAP--TTDYRNTTATGTSALNLPQV-----HAFVNDWASLDMWFSIALMFVCLII 54
Db 560 SIVEPRTTAHANNATQENISTSTNVLTSTAQYISREKKNSTPILQQWFWYLIILVWMI 619

QY 55 IMWLICLKRR-----ARPI 71

Db 620 FVLIFISLRPRREESVPPKPPV 644

RESULT 12

S52920

disintegrin (EC 3.4.24.-) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 06-Jun-1995 #sequence_revision 21-Jul-1995 #text_change 15-Mar-2004

C:Accession: S52920; PC4265

R:Howard, L.; Lu, X.; Mitchell, S.; Griffiths, S.; Glynn, P.

submitted to the EMBL Data Library, March 1995

A:Description: Molecular cloning of MADM: a catalytically active mammalian disintegrin-

A:Reference number: S52920

A:Accession: S52920

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-491 <HOW>

A:Cross-references: UNIPARC:UPI0000150908; EMBL:Z48579

R:McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,

Biochem. Biophys. Res. Commun. 230, 335-339, 1997

A:Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM

A:Reference number: PC4263; MUID:97168971; PMID:9016778

A:Accession: PC4265

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-247 <MCK>

A:Cross-references: UNIPARC:UPI000017C0E0

A:Experimental source: articular chondrocyte

C:Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m

C:Keywords: hydrolase; metalloproteinase

F:126-136/Domain: metal-binding #status predicted <MEB>

F:199-289/Domain: disintegrin homology <DIS>

Query Match 12.28; Score 67; DB 2; Length 491;

Best Local Similarity 23.5%; Pred. No. 14;

Matches 27; Conservative 17; Mismatches 27; Indels 44; Gaps 6;

QY 2 TGSTI-----APTIDYRN-----TTATG-----LTSALNLPQVHAFVNDWASLDMW 42
Db 363 SGRITITLQSPCNDFGVCDFVRCRLVDADGFLARLKAIFSPELYENIAEW--IVAH 420

QY 43 WFSIALMFVCLIIIMWL-----IC-----CLKRRRARPPIVRP 74

Db 421 WVAALLMGIALIMLMAGFIKICSVHTSSNPKLPPPKPLPGLTKRRRPPQIQP 475

RESULT 13

A46103

transmembrane glycoprotein G - Mokola virus

C:Species: Mokola virus

C:Date: 07-Apr-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

A:Reference number: A46103; D46104

R:Tordo, N.; Bourhy, H.; Sather, S.; Ollo, R.

Virology 194, 59-69, 1993

A:Title: Structure and expression in baculovirus of the Mokola virus glycoprotein: an ef

A:Reference number: A46103; MUID:93242783; PMID:8480429

A:Accession: A46103

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-522 <TOR>

A:Cross-references: UNIPROT:Q89507; UNIPARC:UPI00000F7438; GB:S59447; NID:G299713; PIDN:J

R:Bourhy, H.; Kissi, B.; Tordo, N.

Virology 194, 70-81, 1993

A:Title: Molecular diversity of the Lysavirus genus.

A:Reference number: A46104; MUID:93242784; PMID:8386891

A:Contents: lysavirus serotype 3

A:Accession: D46104

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-522 <BOU>

A:Cross-references: UNIPARC:UPI00000F7438; GB:S59448; NID:G299715; PIDN:AAB26296.1; PID:G

A:Note: sequence extracted from NCBI backbone (NCBIN:130542, NCBIP:130548)

C:Superfamily: rabies virus spike glycoprotein

Query Match 12.2%; Score 67; DB 2; Length 522;

Best Local Similarity 33.3%; Pred. No. 15;

Matches 17; Conservative 9; Mismatches 19; Indels 6; Gaps 2;

QY 24 LNLPOVHAFVNDW-ASLDMWF-----SIALMFVCLIIIMWLICLKRRRAR 68

Db 437 LHMPDVHKSVDVLDGLPHWGMILGATIVAFVVLVCLLRVCKRVRERR 487

RESULT 14

T19416

hypothetical protein E01G6.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T19416; T20408

R:Wilkinson, J.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19121

A:Accession: T19416

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-533 <WIL>

A:Cross-references: UNIPROT:O17592; UNIPARC:UPI000007A484; EMBL:Z78416; PIDN:CAB01683.1;

A:Experimental source: clone C23H4

R:Lloyd, C.

submitted to the EMBL Data Library, February 1996

A:Reference number: Z19270

A:Accession: T20408

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-533 <WIL>

A:Cross-references: UNIPARC:UPI000007A484; EMBL:Z69717; PIDN:CAA93533.1; GSPDB:GN00028;

A:Experimental source: clone E01G6

C:Genetics:

A:Gene: CESP:E01G6.3

A:Map position: X

A:Introns: 14/1; 54/1; 58/3; 125/3; 162/1; 194/1; 234/1; 295/1; 319/1; 354/2; 403/1; 455/

Query Match 12.2%; Score 67; DB 2; Length 533;

Best Local Similarity 30.1%; Pred. No. 16;

Matches 22; Conservative 10; Mismatches 29; Indels 12; Gaps 3;

QY 1 MTGSIAPTIDYRNTTATGLT-----SALNLPQVHAFVNDWASLDMW---WFSIALMFV 51

Db 445 MTAFDREVTRQKTSNGTSITWSPHPPGVILP---TKTNESSSFDISSQWFFAIIVV 501

QY 52 CLIIIMWLICLKRR 64

Db 502 ALILFYLIIVLKR 514

RESULT 15

T48284
 hypothetical protein T22P11.220 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: T48284
 R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24490
 A:Accession: T48284
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-428 <BEV>
 A:Cross-references: UNIPROT:Q9L239; UNIPARC:UPI000000C613; EMBL:AL162971
 A:Experimental source: cultivar Columbia; BAC clone T22P11
 C:Genetics:
 A:Map position: 5
 A:Note: T22P11.220

Query Match 12.1%; Score 66.5; DB 2; Length 428;
 Best Local Similarity 25.0%; Pred.No. 14;
 Matches 15; Conservative 11; Mismatches 21; Indels 13; Gaps 2;
 QY 32 FVNDWASLDMMWFSLMFVCLII---MWLICLK-----RRRARPPYRPIIVL 78
 Db 300 YTQDWVSWNQIFPLADITCCCAIVFAMVMSMCLRETSTDKGKVKLAKLPVLRKFYVL 359

Search completed: January 18, 2006, 19:48:21
 Job time : 18 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:01:31 ; Search time 3753 Seconds
(without alignments)
3827.241 Million cell updates/sec

Title: US-10-822-873-10
Perfect score: 307
Sequence: 1 gatgacggctcaaccatcg.....ttctttacagtattgattaa 307

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: gb_est1:*
 - 2: gb_est2:*
 - 3: gb_est3:*
 - 4: gb_hic:*
 - 5: gb_est4:*
 - 6: gb_est5:*
 - 7: gb_est6:*
 - 8: gb_est7:*
 - 9: gb_gse1:*
 - 10: gb_gse2:*
 - 11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	196	63.8	739	6	CD364758	CD364758 UI-H-FT2-
C 2	40.6	13.2	390	5	BU777756	BU777756 SJEDNF08
C 3	40	13.0	533	2	BF272879	BF272879 GA_EB001
C 4	38.8	12.6	648	8	DT112306	DT112306 JGI_ANN01
C 5	38.4	12.5	573	1	AW187495	AW187495 BNLGH1587
C 6	38.4	12.5	856	7	CO122313	CO122313 GR_EB030
C 7	38.4	12.5	865	7	CO116311	CO116311 GR_EB018
C 8	38.2	12.4	571	10	AG974323	AG974323 Drosophila
C 9	37.6	12.2	598	8	CV926006	CV926006 R040C12
C 10	36.8	12.0	754	9	BZ997163	BZ997163 PUGFJ11TD
C 11	36.8	12.0	802	10	CG401905	CG401905 ZMMBB024
C 12	36.8	12.0	882	9	CC401331	CC401331 PUHFL42TD
C 13	36.8	12.0	956	10	CG882662	CG882662 ZMMBB049
C 14	36.4	11.9	768	10	BX214284	BX214284 Danio rerio
C 15	36.4	11.9	991	10	CZ959245	CZ959245 304628 To
C 16	36.2	11.8	331	8	CV949172	CV949172 Pvrpbv_13
C 17	36.2	11.8	701	8	CV959926	CV959926 Pvrpbv_81
C 18	36.2	11.8	1025	10	CL990781	CL990781 ZMMBB000
C 19	36	11.7	562	11	TA303004P	TA303004P T. brucei
C 20	36	11.7	565	9	BH757271	BH757271 BMEAC347H
C 21	35.8	11.7	747	5	EX757054	EX757054 BX757054
C 22	35.6	11.6	582	8	CV951066	CV951066 Pvrpbv_47

C 23	35.6	11.6	627	10	CW336158	CW336158 104_835_1
C 24	35.6	11.6	693	10	CW296187	CW296187 104_777_1
C 25	35.6	11.6	699	10	CW427119	CW427119 fbb5001f1
C 26	35.6	11.6	734	10	BX155641	BX155641 Danio rer
C 27	35.4	11.5	845	8	CV907775	CV907775 PDpced 27
C 28	35.2	11.5	686	6	CD845789	CD845789 DH0AB0062
C 29	35	11.4	364	1	AI573060	AI573060 tr69a09.x
C 30	35	11.4	645	9	BZ899030	BZ899030 CH240_158
C 31	35	11.4	713	8	CX602294	CX602294 CT02032A2
C 32	34.8	11.3	137	9	BH261969	BH261969 CH230-177
C 33	34.8	11.3	626	9	BH275362	BH275362 CH230-177
C 34	34.8	11.3	730	10	BX140275	BX140275 Danio rer
C 35	34.8	11.3	741	6	CF446046	CF446046 EST682391
C 36	34.4	11.2	195	10	CL279542	CL279542 Ggal_93d
C 37	34.4	11.2	704	9	BZ193754	BZ193754 CH230-269
C 38	34.4	11.2	786	9	BH733089	BH733089 BOMBF75TR
C 39	34.2	11.1	553	10	CE614912	CE614912 tigr-g88-
C 40	34.2	11.1	706	8	CV906572	CV906572 PDpced 14
C 41	34.2	11.1	710	5	BX269320	BX269320 BX269320
C 42	34.2	11.1	758	10	AG536301	AG536301 Mus muscu
C 43	34.2	11.1	844	7	CK160091	CK160091 FGAS04163
C 44	34	11.1	184	6	CF685536	CF685536 CCACU16TR
C 45	34	11.1	246	1	AA051869	AA051869 Cn0055-5

ALIGNMENTS

RESULT 1
LOCUS CD364758/c
DEFINITION UI-H-FT2-bjm-j-05-0-UI.s1 NCI CGAP_FT2 Homo sapiens CDNA clone
ACCESSION CD364758
VERSION CD364758.1 GI:31148848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 739)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source

Location/Qualifiers
1..739
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FT2-bjm-j-05-0-UI"
/tissue_type="Alveolar Macrophage"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP_FT2"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage)

(some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UT-H-FT2
TAG_SEQ=GGCCATGCGG"

ORIGIN

Query Match 63.8%; Score 196; DB 6; Length 739;
Best Local Similarity 86.4%; Pred. No. 1.2e-50;
Matches 228; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 45 CCACCTGCTACCGGACTAACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATG 104
DB 307 CCGCGCTACCGGACTTACATCTACCAACAATACACCCCAAGTTTCGCTTTGTCAATG 248

QY 105 ACTGGCGAGCTTGGACATGTGGTGTTCATAGCGCTTATGTTTGGCTTATTA 164
DB 247 ACTGGGATACTTGGCATGTGGTGTTCCTCATAGCGCTTATGTTTGTATGCTTATTA 188

QY 165 TTATGGCTTATTTGTTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTA 224
DB 187 TTATGGCTCATCTGCTGCTAAAGCGCAACGCGCCGACCCCATCTATAGTCCCA 128

QY 225 TCATTGTGCTCAACCCACACAAATGAAAATTCATAGATTGGAGGTCGAAC-CATGT 283
DB 127 TCATTGTGCTACACCCAAACAATGGAATCCATAGATTGGAGGACTGAACACATGT 68

QY 284 TCTCTCTTTTACAGTATGATTA 307
DB 67 TCCTTCTTACAGTATGATTA 44

RESULT 2

BU777756/c
LOCUS BU777756 390 bp mRNA linear EST 23-OCT-2003
DEFINITION SJEDNF08 SJE Schistosoma japonicum cDNA, mRNA sequence.
ACCESSION BU777756
VERSION BU777756.1 GI:28345072
KEYWORDS EST.
SOURCE Schistosoma japonicum
ORGANISM Schistosoma japonicum
REFERENCE 1 (bases 1 to 390)
AUTHORS Hu, W., Yan, Q., Shen, D. K., Liu, F., Zhu, Z. D., Song, H. D., Xu, X. R., Wang, Z. J., Rong, Y. P., Zeng, L. C., Wu, J., Zhang, X., Wang, J. J., Xu, X. N., Wang, S. Y., Fu, G., Zhang, X. L., Wang, Z. Q., Brindley, P. J., McManus, D. P., Xue, C. L., Feng, Z., Chen, Z. and Han, Z. G.
TITLE Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource
JOURNAL Nat. Genet. 35 (2), 139-147 (2003)
PUBMED 12973349
COMMENT Contact: Zequang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn.

FEATURES

source

Location/Qualifiers
1..390
/organism="Schistosoma japonicum"
/mol_type="mRNA"
/db_xref="taxon:6182"
/tissue_type="Whole egg"
/dev_stage="egg"
/lab_host="rabbits"
/clone_lib="SJB"

ORIGIN

Query Match 13.2%; Score 40.6; DB 5; Length 390;
Best Local Similarity 52.7%; Pred. No. 0.18;
Matches 88; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 133 TTCCATAGCGCTATCTTTGTTGCTTATTATATGCTTATGTTGCTTAAAGCG 192
DB 327 TTGGTTAGGAGCTGTATTAATCAGTTGACATAAGTTACTGATTGTTTGTATCAATTG 268

QY 193 CAGACGCGCAGACACCCCATCTATAGGCTCATCTTGTGCTCAACCCACACAATGAAAA 252
DB 267 GTCAAAACACAGATCACTCAGTTATCTGATGAGATCATCTCGGCAATAATTCAGACAA 208

QY 253 AATTCATAGATTGAGCGGTCTGAACCATGTTCTCTTCTTTTACAGT 299
DB 207 AATTTATGATCTCGCGGATATGAACCAATGTTTTTTAGTTTTCAGT 161

RESULT 3

LOCUS

BF272879 533 bp mRNA linear EST 07-MAR-2001
GA_Eb0016C17f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Eb0016C17f, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gossypium arboreum
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 533)
Wing, R. A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T. C., Leslie, A. and Wilkins, T. A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber

JOURNAL

COMMENT

Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11203949.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Seq primer: TAATACGACTCACTATAGGG

High quality sequence stop: 522.

FEATURES

source

Location/Qualifiers
1..533
/organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Eb0016C17f"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Query Match 13.0%; Score 40; DB 2; Length 533;
 Best Local Similarity 55.9%; Pred. No. 0.29;
 Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 97 TGTCATGACTGGCGAGCTTGACATGTGGTGTTCATAGCGCTTATGTTGTTG 156
 |||||
 Db 82 TTCTATTAAGAGCTGCGCTTTAACAGGTGAAGCCAGTGAAGAGTGTTCATTTGTTGG 141
 |||||

QY 157 CCTATTATATATGCTTATTTGTTGCTTAAGCGCAGACGCGCAGACCCCCCACTTA 216
 |||||
 Db 142 AATTGCTGGAATGTTCCATATGCGATCCACAGTCGAGTTCAGCCTGAACCCCACTTA 201
 |||||

QY 217 TAGSCCTATCATGTG 232
 |||||
 Db 202 TATGCACATCCTTCTG 217
 |||||

RESULT 4
 DT112306/c 648 bp mRNA linear EST 12-AUG-2005
 LOCUS JGI_ANNO1937.rev ANNO Pimephales promelas whole (M) Pimephales
 DEFINITION promelas cDNA clone ANNO1937 3', mRNA sequence.
 DT112306
 DT112306.1 GI:72470750
 EST.
 Pimephales promelas
 ORGANISM Pimephales promelas
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Pimephales.
 1 (bases 1 to 648)
 Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C.,
 Brokstein, P., and Lindquist, E.A.
 DOE Joint Genome Institute Pimephales promelas EST project
 Unpublished (2005)
 Other ESTs: JGI ANNO1937.fwd
 Contact: Lindquist, E.A., Richardson, P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 CDNA Library Preparation: DOE Joint Genome Institute:
 http://www.jgi.doe.gov
 DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
 Naming Conventions: EST name is generated by the concatenation of
 the JGI Clone Id and the direction of sequencing. The suffix '.rev'
 indicates a reverse sequencing read of the insert. It does not
 necessarily reflect the orientation of the insert.
 Poly-A: Based upon the presence of a run of 14 or more T residues
 at the beginning of the sequence, this clone was polyadenylated.
 The resulting Poly-T sequence has been removed.
 Plate: ANNO 0021 row: a column: 5
 High quality sequence stop: 553
 POLYA=Yes.

FEATURES
 source
 1..648
 Location/Qualifiers
 /organism="Pimephales promelas"
 /mol_type="mRNA"
 /db_xref="taxon:90988"
 /clone="ANNO1937"
 /tissue_type="Whole"
 /dev_stage="Adult"
 /clone_lib="ANNO Pimephales promelas Whole (M)"
 /note="Vector: pDONR222. The library was made from dT
 primed cDNA and cloned into Invitrogen vector pDONR222.
 Poly A RNA were primed with a Biotin-attB2-Oligo(dT)
 primer (5'- GGCGCGCCGACAACTTTGTACAGAAAGTTGGT (T)19 -3')
 and the first strand synthesized using Superscript II
 (Invitrogen). The second strand was synthesized and an
 attB1 adaptor was ligated to the 5' end (5'-
 TCGTCGGGCACTTTGTACAAAAGTTGCCC -3' and 5'-
 CCAACTTTTGTACAAAAGTTGCCCC -3'). The cDNA was size

selected using 1% agarose gel electrophoresis. (L
 ~0.5-1.2k, M ~1.2-2.5k, H ~2.5k) and then inserted into
 the vector using site specific recombination (flanking
 attB sites on cDNA). The work was done at DOE Joint Genome
 Institute."

ORIGIN
 Query Match 12.6%; Score 38.8; DB 8; Length 648;
 Best Local Similarity 64.4%; Pred. No. 0.73;
 Matches 58; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 98 GTCAATGACTGGCGAGCTTGACATGTGGTGTTCATAGCGCTTATGTTGTTG 157
 |||||
 Db 158 GTCGATGTCAGGCTTGACTGGACATGTAGTTGTTCCCTTTCTTCCATTTGTCG 99
 |||||

QY 158 CTTATTATTATGTCGCTTATTTGTCCTA 187
 |||||
 Db 98 CTTATTATTATGTCGCTTATTTGTTAATA 69
 |||||

RESULT 5
 AW187495
 LOCUS BNLGHI5871 Six-day Cotton fiber Gossypium hirsutum cDNA 5', mRNA
 DEFINITION
 AW187495
 AW187495.1 GI:6461931
 EST.
 Gossypium hirsutum (upland cotton)
 ORGANISM Gossypium hirsutum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 1 (bases 1 to 573)
 Blewitt, M., Matz, E.C. and Burr, B.
 ESTs from developing cotton fiber (1999b)
 Unpublished (1999)
 Contact: Ben Burr
 Biology Department
 Brookhaven National Laboratory
 Upton, NY 11973, USA
 Tel: 516-344-3396
 Fax: 516-344-3407
 Email: burr@bnl.bnl.gov
 Seq primer: T3 Primer.
 Location/Qualifiers
 1..573
 /organism="Gossypium hirsutum"
 /mol_type="mRNA"
 /cultivar="Acala Maxxa"
 /db_xref="taxon:3635"
 /tissue_type="immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="XLI-Blue"
 /clone_lib="Six-day Cotton fiber"
 /note="Vector: pBluescript II KS+"

FEATURES
 source
 1..573
 Location/Qualifiers
 /organism="Gossypium hirsutum"
 /mol_type="mRNA"
 /cultivar="Acala Maxxa"
 /db_xref="taxon:3635"
 /tissue_type="immature fiber"
 /dev_stage="Six days post anthesis"
 /lab_host="XLI-Blue"
 /clone_lib="Six-day Cotton fiber"
 /note="Vector: pBluescript II KS+"

ORIGIN
 Query Match 12.5%; Score 38.4; DB 1; Length 573;
 Best Local Similarity 55.1%; Pred. No. 0.95;
 Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 97 TGTCAATGACTGGCGAGCTTGACATGTGGTGTTCATAGCGCTTATGTTGTTG 156
 |||||
 Db 363 TTCTATTAGGAGCTGCGCTTTAACAGGTGAAGCCAGTGAAGAGTGTTCATTTGTTGG 422
 |||||

QY 157 CTTATTATTATGTCGCTTATTTGTTGCTTAAGCGCAGACGCGCAGACCCCCCACTTA 216
 |||||
 Db 423 AATTGCTGGAATGTTCCATATGCGATCCACAGTCGAGTTCAGCCTGAACCCCACTTA 482
 |||||

QY 217 TAGGCTATCATGTG 232
 |||||
 Db 483 TATGCACATCCTTCTG 498
 |||||

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RESULT 6
LOCUS      C0122313
DEFINITION GR_EB03001.f GR_Eb Gossypium raimondii cDNA clone GR_EB03001 5',
            mRNA sequence.
ACCESSION  C0122313
VERSION    C0122313.1 GI:48821000
KEYWORDS   EST.
SOURCE     Gossypium raimondii
ORGANISM   Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

REFERENCE  1 (bases 1 to 856)
AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
            Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
            Wing,R.A.
TITLE     Global assembly of Cotton ESTs
JOURNAL   Unpublished (2004)
COMMENT   Contact: Rod A. Wing
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            Plate: 018 row: I column: 06.

FEATURES   source
            Location/Qualifiers
            1..856
               /organism="Gossypium raimondii"
               /mol_type="mRNA"
               /db_xref="taxon:29730"
               /clone="GR_EB018106"
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               /lab_host="DH10B"
               /clone_lib="GR_Eb"
               /note="vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
               EcoRV; Library made by Invitrogen with RNA supplied by
               Wendle lab. Directional cloned into NotI-EV. Colonies
               plated/picked by AGI. More glycerol clones held in -80."

ORIGIN
Query Match      12.5%; Score 38.4; DB 7; Length 856;
Best Local Similarity 55.1%; Pred. No. 1;
Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy  97  TGTCAATGACTGGCGAGCTTGGACATGTGGTGTTCATAGCGCTTATGTTGTTG 156
Db  237  TTCTATTAGAGCTGGCTTTACAGGTGACGAGTGAAGAGTGTTCATTTGTTGG 296

Qy  157  CCTATTATTATGTCCTTATTTGTCCTTAAGCCGACGCGCCAGACCCCATCTA 216
Db  297  AATTGCTGGAATGTTCCATATCGCATCCACGAGTCGAGTTCAGCTGGACCCCACTTA 356

Qy  217  TAGGCCTATCATTTGTG 232
Db  357  TATGCACATCCTCTG 372

RESULT 8
LOCUS      AG974323
DEFINITION Drosophila simulans DNA, clone: DSM1-015001.F.fa, genomic survey
            sequence.
ACCESSION  AG974323
VERSION    AG974323.1 GI:58523216
KEYWORDS   GSS.
SOURCE     Drosophila simulans
ORGANISM   Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  1
AUTHORS   Hattori,M., Toyoda,A., Murakami,K., Kuroki,Y., Fujiyama,A.,
            Toshio,T.K. and Sakaki,Y.
TITLE     BAC end sequences of Library DNB1
JOURNAL   Unpublished
COMMENT   2 (bases 1 to 571)
            Hattori,M.
            Direct Submission
            Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 865)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wing,R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 018 row: I column: 06.

FEATURES   source
            Location/Qualifiers
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               /organism="Gossypium raimondii"
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               /clone_lib="GR_Eb"
               /note="vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
               EcoRV; Library made by Invitrogen with RNA supplied by
               Wendle lab. Directional cloned into NotI-EV. Colonies
               plated/picked by AGI. More glycerol clones held in -80."

ORIGIN
Query Match      12.5%; Score 38.4; DB 7; Length 865;
Best Local Similarity 55.1%; Pred. No. 1;
Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy  97  TGTCAATGACTGGCGAGCTTGGACATGTGGTGTTCATAGCGCTTATGTTGTTG 156
Db  237  TTCTATTAGAGCTGGCTTTACAGGTGACGAGTGAAGAGTGTTCATTTGTTGG 296

Qy  157  CCTATTATTATGTCCTTATTTGTCCTTAAGCCGACGCGCCAGACCCCATCTA 216
Db  297  AATTGCTGGAATGTTCCATATCGCATCCACGAGTCGAGTTCAGCTGGACCCCACTTA 356

Qy  217  TAGGCCTATCATTTGTG 232
Db  357  TATGCACATCCTCTG 372

RESULT 8
LOCUS      AG974323
DEFINITION Drosophila simulans DNA, clone: DSM1-015001.F.fa, genomic survey
            sequence.
ACCESSION  AG974323
VERSION    AG974323.1 GI:58523216
KEYWORDS   GSS.
SOURCE     Drosophila simulans
ORGANISM   Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  1
AUTHORS   Hattori,M., Toyoda,A., Murakami,K., Kuroki,Y., Fujiyama,A.,
            Toshio,T.K. and Sakaki,Y.
TITLE     BAC end sequences of Library DNB1
JOURNAL   Unpublished
COMMENT   2 (bases 1 to 571)
            Hattori,M.
            Direct Submission
            Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 865)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wing,R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 018 row: I column: 06.

FEATURES   source
            Location/Qualifiers
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               /organism="Gossypium raimondii"
               /mol_type="mRNA"
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               /tissue_type="floral"
               /dev_stage="3 to +3 DPA"
               /lab_host="DH10B"
               /clone_lib="GR_Eb"
               /note="vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
               EcoRV; Library made by Invitrogen with RNA supplied by
               Wendle lab. Directional cloned into NotI-EV. Colonies
               plated/picked by AGI. More glycerol clones held in -80."

ORIGIN
Query Match      12.5%; Score 38.4; DB 7; Length 856;
Best Local Similarity 55.1%; Pred. No. 1;
Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy  97  TGTCAATGACTGGCGAGCTTGGACATGTGGTGTTCATAGCGCTTATGTTGTTG 156
Db  370  TTCTATTAGAGCTGGCTTTACAGGTGACGAGTGAAGAGTGTTCATTTGTTGG 429

Qy  157  CCTATTATTATGTCCTTATTTGTCCTTAAGCCGACGCGCCAGACCCCATCTA 216
Db  430  AATTGCTGGAATGTTCCATATCGCATCCACGAGTCGAGTTCAGCTGGACCCCACTTA 489

Qy  217  TAGGCCTATCATTTGTG 232
Db  490  TATGCACATCCTCTG 505

RESULT 7
LOCUS      C0116311
DEFINITION GR_EB018106.r GR_Eb Gossypium raimondii cDNA clone GR_EB018106
            3', mRNA sequence.
ACCESSION  C0116311
VERSION    C0116311.1 GI:48814998
KEYWORDS   EST.
SOURCE     Gossypium raimondii
ORGANISM   Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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DEFINITION ZM9990492E18f ZM9990492E18f Zea mays genomic clone
ACCESSION ZM9990492E18 5', genomic survey sequence.
VERSION CG882662
KEYWORDS GSS.
SOURCE CG882662.1 GI:38613671
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 956)
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zohovetz, V., Fuks, G., Yu, Y., Wang, R. and Messing, J.
Sequencing of the maize genome at FGI (2003c)
Unpublished (2003)
Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 86.
Location/Qualifiers
source 1..956
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/mol_type="genomic DNA"
/cultivar="B73"
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/lab_host="E. coli DH10B"
/clone_lib="ZM9990492E18"
/notes="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

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Best Local Similarity 50.0%; Pred. No. 3.3;
Matches 92; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 123 TGTGTTGTTTTCATAGCGCTTATGTTTGGCTTATATATATATATGCTTATTTGTT 182
Db 127 TTTTGTCTTGTCACTAATTTGTTTTCATATTTTTCGTTATGCTGCTGATTTATC 186
QY 183 GCCTAAGCGCAGCGCGCGAGACCCCATCTATAGGCTTATGCTCAACCCAC 242
Db 187 CGTCCAAATTTATTTTGTGAGACTTCCGAGCGAGAGCTATTTTTCGCGAGAAA 246
QY 243 ACAATGAAATTTATAGATTCGAGCGCTGAAACCATGTTCTCTCTTTTACAGTATG 302
Db 247 GAAATATAGCATAACAAATAGTTTGAAGAGGTAACCTGAATTTTCTATTTATCTC 306
QY 303 ATTA 306
Db 307 ATTA 310

RESULT 14
BX214284/c
LOCUS BX214284 768 bp DNA linear GSS 29-JAN-2003
DEFINITION Danio rerio genomic clone DKEY-258E20, genomic survey sequence.
ACCESSION BX214284
VERSION BX214284.1 GI:28046170
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 768)
Humphray, S.J., Huckle, E. and Durham, J.L.

DEFINITION Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 258E20. 258E20
is part of the Daniokey BAC Library created by R. Piasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
source 1..768
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-258E20"
/tissue_type="testis"
/notes="vector pindigobAC-536"

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Best Local Similarity 52.7%; Pred. No. 4.3;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 113 AGCTTCGACATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTATATATATATGTTG 172
Db 231 ACCTTAAGATGATAGTATTTAATAGTCGTATGCTATTTGCATTTATATGATTTA 172
QY 173 CTTATTTTGTGCTAAAGCGCAGACGCCGACATCTATAGGCTTATAGGCTTATATGTTG 232
Db 171 TATAATCGTTATATATATATGCGGATAGATGATCTCAAAATTAAGTATATCGCTTAT 112
QY 233 CTCACCCACACATGCAAAAATTCATAGA 262
Db 111 CGCAGCAATGTCTATGACAAATATCACACA 82

RESULT 15
CZ959245/c
LOCUS CZ959245 991 bp DNA linear GSS 11-AUG-2005
DEFINITION 304628 Tomato EcorI BAC Library Lycopersicon esculentum genomic
clone SL EcorI0001113 3, genomic survey sequence.
ACCESSION CZ959245
VERSION CZ959245.1 GI:72310041
KEYWORDS GSS.
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 991)
Mueller, L.A., Buel, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J.,
Van Eck, J. and Stack, S.
BAC end sequencing from three Solanum lycopersicon libraries
Unpublished (2005)
Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant Breeding
Cornell University
251 Emerson Hall, Ithaca, NY 14853, USA
Tel: 607-255-6557
Fax: 607-255-6683
Email: sgn-feedback@sgn.cornell.edu
Plate: 1 row: 1 column: 13
Seq primer: SP6
Class: BAC ends
High quality sequence start: 27
High quality sequence stop: 694.
Location/Qualifiers
source 1..991
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="Heinz 1706"
/db_xref="taxon:4081"
/clone="SL_EcorI0001113"
/lab_host="E. coli"

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/clone lib="Tomato EcoRI BAC Library"
/note="Vector: unk; Site_1: EcoRI"

ORIGIN

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Best Local Similarity 55.6%; Pred. No. 4.5;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy      142 GCTTATCTTTGTTGGCTTATTATTATGTTGGCTTATTGTTGGCTTAAAGCGCAGACGCGC 201
Db      406 GTTTTGTAGGTTGCGAGGTTTAATATCATGCATATATTTTGTATCTATCGTTCAAGGGG 347

Qy      202 CAGACCCCATCTATAGGCTATCATTTGTGCTCAACCCACACAATGAAAAAATTCATAG 261
Db      346 TGAACCTCCATCATCAAACTCTTGTATGATCNAATCATCAGGAGCAGAAAAATATAA 287

Qy      262 ATTGGA 267
Db      286 TTGTGA 281
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Search completed: January 20, 2006, 21:07:43
Job time : 3759 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 19:42:01 ; Search time 77 Seconds

(without alignments)
576.328 Million cell updates/sec

Title: US-10-822-873-11

Perfect score: 551

Sequence: 1 MTGSTTAPTDTYRNTATGL.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	100.0	101	2	AAW61197
2	551	100.0	101	2	AAW78902
3	551	100.0	101	2	AAW75787
4	551	100.0	101	2	AAW98003
5	551	100.0	101	3	AAW84407
6	551	100.0	101	4	AAW61866
7	551	100.0	101	4	AAW50206
8	551	100.0	101	4	AAW47591
9	551	100.0	101	5	ABG69353
10	551	100.0	101	6	ABU10308
11	551	100.0	101	8	ADI36347
12	551	100.0	101	9	ADV20979
13	551	100.0	101	9	ADW47775
14	547	99.3	101	2	AAW59925
15	545	98.9	101	9	ADW28321
16	459	83.3	95	4	AAW61868
17	458	83.1	87	4	AAW61870
18	428.5	77.8	84	4	AAW61872
19	422	76.6	78	4	AAW61869
20	395	71.7	77	4	AAW61871
21	372	67.5	94	4	AAW61865
22	346	62.8	93	4	AAW61867
23	233	42.3	42	4	AAW61876
24	209	37.9	40	4	AAW61873

RESULT 1

ID	AAW61197	standard; protein; 101 AA.
XX	XX	
AC	AAW61197;	
XX	XX	
DT	27-AUG-2003	(revised)
DT	07-DEC-1998	(first entry)
XX	XX	
DE	Adenovirus death protein.	
XX	XX	
KW	Adenovirus death protein; ADP; vector; hepatoma; cancer;	
KW	alpha-fetoprotein transcription regulatory element; AFP-TRD;	
KW	hepatocellular carcinoma; hepatoma; gene therapy; human.	
XX	XX	
OS	Mastadenovirus.	
XX	XX	
PN	W09839465-A2.	
XX	XX	
PD	11-SEP-1998.	
XX	XX	
PF	03-MAR-1998;	98WO-US004084.
XX	XX	
PR	03-MAR-1997;	97US-0039597P.
PR	02-MAR-1998;	98US-00033428.
XX	XX	
PA	(CALY-) CALYDON INC.	
XX	XX	
PI	Little AS, Lamparski HG, Henderson DR, Schuur ER, WPI; 1998-495861/42.	
XX	XX	
DR	N-PSDB; AAV47675.	
XX	XX	
PT	New adenovirus vector, for treating cancers - comprising an adenovirus gene under the transcriptional control of an alpha fetoprotein transcription regulatory element.	
XX	XX	
PS	Claim 29; Page 74; 102pp; English.	
XX	XX	
CC	This is the amino acid of the adenovirus death protein (ADP) of of adenovirus type 2. The ADP coding sequence (see AAV47675), with or without the Y leader, can be introduced into an adenoviral genome, e.g. in the E3 or E4 region. Inclusion of such a coding sequence in an CC adenoviral vector significantly enhances the extent of cytotoxicity, cell CC killing and virus production. The invention provides replication-competent adenovirus vectors which preferentially replicate in cells that CC express alpha-fetoprotein (AFP), particularly hepatoma cells. The vectors	

ALIGNMENTS

25	109	19.8	19	4	AAW61874
26	76	13.8	172	9	ADZ13436
27	74	13.4	544	7	ADD45030
28	73.5	13.3	521	7	ABO63032
29	72	13.1	1248	8	ABM83572
30	72	13.1	1274	8	ABM83571
31	71	12.9	199	8	ADQ66329
32	71	12.9	199	9	ADZ13434
33	71	12.9	239	6	ABU60695
34	71	12.9	277	3	AAW79207
35	71	12.9	277	6	ABU60694
36	71	12.9	277	7	ADP50686
37	71	12.9	282	8	ABM82908
38	71	12.9	282	8	ABM82910
39	71	12.9	282	8	ABM82909
40	71	12.9	282	8	ABM82911
41	71	12.9	282	8	ABM82912
42	71	12.9	283	2	AAW05809
43	71	12.9	283	2	AAW12659
44	71	12.9	283	2	AAW60045
45	71	12.9	283	2	AAW69238

Aab61874 Ad2 ADP t
Adz13436 Human can
Add45030 Rat Prote
Abo63032 Klebsiell
Abm83572 Human dia
Abm83571 Human dia
Adq66329 Novel hum
Adz13434 Human can
Aab60695 Human mat
Aay79207 Membrane-
Abu60694 Human mem
Adf50686 Soluble f
Abm82908 Human dia
Abm82910 Human dia
Abm82909 Human dia
Abm82911 Human dia
Abm82912 Human dia
Aaw05809 Human tum
Aaw12659 Human her
Aaw60045 Human TNF
Aaw69238 Herpesvir

Db 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLOYD 101

RESULT 4

AAW98003
ID AAW98003 standard; protein; 101 AA.
XX
AC AAW98003;
XX
XX 17-OCT-2003 (revised)
DT 21-JUN-1999 (first entry)
XX
XX Adenovirus death protein.
XX
XX Enhancer; glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer;
KW therapy; adenovirus death protein.
XX
XX Human adenovirus type 2.
OS
XX W09906576-A1.
FN
XX
XX 11-FEB-1999.
PD
XX
XX 04-AUG-1998; 98WO-US016312.
PF
XX
XX 04-AUG-1997; 97US-0054523P.
PR
XX 02-MAR-1998; 98US-0076545P.
PR
XX 03-AUG-1998; 98US-00127834.
PR
XX
XX (CALY-) CALYDON INC.
PA
XX
XX Yu D, Herdenson DR, Schuur ER;
PI
XX WPI; 1999-153804/13.
DR
XX N-PSDB; AAX24756.
DR
XX
XX New nucleic acid containing the human glandular kallikrein enhancer -
PT providing increased expression of heterologous sequences in prostatic
PT cells, and related adenoviral vectors for treating prostatic cancer.
PT
XX
XX Disclosure; Page 165-166; 179pp; English.
PS
XX

CC This protein comprises the adenovirus death protein (ADP) of adenovirus
CC serotype 2. The invention provides novel adenovirus vectors in which at
CC least one adenovirus gene, preferably one that contributes to
CC cytotoxicity, is placed under transcriptional control of a human
CC glandular kallikrein hKLK2 enhancer transcriptional regulatory element
CC (hKLK2-TRE, see AAX24755). Such vectors are useful for treatment of
CC cancers such as prostate cancer. The ADP gene may render the adenoviral
CC vector more potent, making possible more effective treatment and/or lower
CC dosage requirement. (Updated on 17-OCT-2003 to standardise OS field)
CC
XX
SQ Sequence 101 AA;

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-61;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Qy 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLOYD 101

RESULT 5
AAW84407
ID AAW84407 standard; protein; 101 AA.
XX
AC AAW84407;

XX
DT 25-JUL-2000 (first entry)
XX
XX Amino acid sequence of an adenoviral death protein.
XX
XX adenoviral vector; adenovirus gene; transcriptional control;
KW transcriptional regulatory element; TRE; adenoviral propagation;
KW death protein; tumour.
XX
XX Mastadenovirus.
OS
XX W0200015820-A1.
PN
XX
XX 23-MAR-2000.
PD
XX
XX 10-SEP-1999; 99WO-US020718.
PF
XX
XX 10-SEP-1998; 98US-0099791P.
PR
XX 09-SEP-1999; 99US-00392822.
PR
XX (CALY-) CALYDON INC.
PA
XX
XX Yu DC, Henderson DR;
PI
XX WPI; 2000-271456/23.
DR
XX N-PSDB; AAZ99937.
DR
XX
XX Adenovirus vectors comprising cell-status specific response elements
PT useful in gene therapy protocols for the treatment of cancers.
PT
XX
XX Disclosure; Fig 9; 79pp; English.
PS
XX

CC The present sequence represents an adenoviral death protein, which is
CC used to construct the vectors of the invention. The specification
CC describes adenoviral vectors which comprise an adenovirus gene under
CC transcriptional control of a cell status specific transcriptional
CC regulatory element (TRE). The TRE is preferably one that is essential for
CC adenoviral propagation. The adenovirus vectors may be used for the
CC treatment of a range of tumours such as lung, stomach, breast, colon and
CC rectum, and uterine and cervix cancers
XX
SQ Sequence 101 AA;

Query Match 100.0%; Score 551; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-61;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Qy 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLOYD 101

RESULT 6
AAB61866
ID AAB61866 standard; protein; 101 AA.
XX
AC AAB61866;
XX
XX 08-MAY-2001 (first entry)
DT
XX
XX Ad2 encoded adenovirus death protein (ADP).
DE
XX Adenovirus death protein; ADP; neoplastic; cell death; cancer therapy;
KW anti-cancer; gene therapy; cytostatic; Ad2.
KW
XX Mastadenovirus.
OS
XX
XX Key Location/Qualifiers
FH Domain 1. .40
FT

FT Peptide /note= "putative luminal domain (AAB61873)"
 FT 1..26
 FT /note= "fragment specifically claimed for"
 FT Domain 41..59
 FT /note= "transmembrane domain (AAB61874); fragment
 FT specifically claimed for"
 FT Domain 60..101
 FT /note= "cytoplasmic-nucleoplasmic domain"
 FT Domain 63..70
 FT /note= "cytosolic basic proline domain (AAB61875)
 FT fragment specifically claimed for"
 XX WO200104282-A2.
 XX 18-JAN-2001.
 XX 12-JUL-2000; 2000WO-US018971.
 XX 12-JUL-1999; 99US-00351778.
 XX (UYSL-) UNIV SAINT LOUIS.
 XX Wold WSM, Toth K, Doronin K, Tollefsen AE;
 XX WPI; 2001-103079/11.
 XX Recombinant vector which is replication-competent in a neoplastic cell
 PT and overexpresses an adenovirus death protein, useful in cancer therapy
 PT when used together with replication-defective adenovirus which expresses
 PT an anti-cancer gene.
 XX Claim 5; Page 156; 196pp; English.
 XX The invention relates to a recombinant vector (VI) which is replication-
 CC competent in a neoplastic cell and which overexpresses an adenovirus
 CC death protein (ADP). The vector can be used in a method for promoting
 CC death of a neoplastic cell that comprises contacting the neoplastic cell
 CC with at least one VI; and a composition comprising VI and a second
 CC recombination virus which is: (a) replication defective and which
 CC expresses an anti-cancer gene product, where VI complements replication
 CC of the second recombinant virus; or (b) replication-competent in a
 CC neoplastic cell. VI, together with one or more replication-defective
 CC adenovirus which expresses an anti-cancer gene product, are useful in
 CC cancer therapy. Overexpression of ADP by VI results in faster lysis of
 CC cells and spread of the virus throughout a cell monolayer than viruses
 CC expressing wild-type levels of ADP. The present sequence represents the
 CC amino acid sequence of an ADP encoded by Ad2
 XX SQ Sequence 101 AA;
 Query Match 100.0%; Score 551; DB 4; Length 101;
 Best Local Similarity 100.0%; Pred. No. 2.5e-61;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSLMVFVCLIIIMWLC 60
 DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSLMVFVCLIIIMWLC 60
 QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
 DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
 RESULT 7
 ID AAM50206
 XX AAM50206 standard; protein; 101 AA.
 XX AAM50206;
 AC AAM50206;
 XX 11-SEP-2003 (revised)
 DT 07-JAN-2002 (first entry)
 XX Adenovirus death protein.
 DE

XX Adenovirus death protein; uroplakin II; vector;
 KW transcriptional regulatory element; TRE; urothelial cell; bladder cancer;
 KW human; gene therapy.
 XX Human adenovirus type 2.
 OS WO200172994-A2.
 PN 04-OCT-2001.
 XX 21-MAR-2001; 2001WO-US009224.
 XX 24-MAR-2000; 2000US-0191861P.
 PR (CALY-) CALYDON INC.
 PA Yu D, Zhang H, Henderson DR;
 XX WPI; 2001-639229/73.
 DR N-PSDB; AAI70186.
 XX Human urothelial cell specific uroplakin transcriptional regulatory
 PT sequences, useful for producing adenoviral vectors which can be used to
 PT confer selective cytotoxicity to target cells, especially bladder cancer
 PT cells.
 XX Example 6; Fig 12; 147pp; English.
 PS The present sequence is that of the adenovirus death protein (ADP). The
 CC ADP gene coding region (see AAI70186) was obtained by PCR amplification
 CC and used in the construction of adenoviral vectors in which ADP
 CC expression was under the control of a urothelial cell-specific
 CC transcriptional regulatory element (TRE) derived from the human uroplakin
 CC II gene 5' flanking region (see AAI70144). This is an example of
 CC adenoviral vectors of the invention. Such vectors comprise a gene,
 CC preferably an adenovirus gene, under transcriptional control of a
 CC urothelial cell-specific TRE. They display urothelial cell-specific
 CC cytotoxicity, and are used for the specific, targeted gene therapy of
 CC bladder cancer. (Updated on 11-SEP-2003 to standardise OS field)
 XX SQ Sequence 101 AA;
 Query Match 100.0%; Score 551; DB 4; Length 101;
 Best Local Similarity 100.0%; Pred. No. 2.5e-61;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSLMVFVCLIIIMWLC 60
 DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSLMVFVCLIIIMWLC 60
 QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
 DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
 RESULT 8
 ID AAB47591
 XX AAB47591 standard; protein; 101 AA.
 XX AAB47591;
 AC AAB47591;
 XX 11-SEP-2003 (revised)
 DT 07-JAN-2002 (first entry)
 XX ADP amino acid sequence.
 DE Adenovirus; ADP; replication-competent; adenoviral vector; TRE;
 KW transcriptional regulatory element; mutation; deletion; IRES; promoter;
 KW internal ribosome entry site; cytotoxic; cancer; bladder.
 XX unidentified adenovirus.
 OS

PN WO200173093-A2.
XX 04-OCT-2001.
XX 21-MAR-2001; 2001WO-US009036.
XX 24-MAR-2000; 2000US-0192156P.
XX (CALY-) CALYDON INC.
XX Yu D, Li Y, Henderson DR;
XX WPI; 2001-639234/73.
XX N-PSDB; AAH43535.
XX Replication-competent adenoviral vector, useful e.g. for killing cancer
XX cells, contains two genes linked by internal ribosome entry site and
XX controlled by target-specific regulator.
XX Disclosure; Fig 9; 148pp; English.
XX This sequence represents adenoviral ADP. The ADP coding sequence may be
XX used in the replication-competent adenoviral vector (A) of the invention
XX which contains two genes (G1, G2) that are co-transcribed as a single
XX mRNA and under control of a heterologous, target cell- specific
XX transcriptional regulatory element (TRE). G2 has a mutation in, or
XX deletion of, its endogenous promoter and is controlled from an internal
XX ribosome entry site (IRES). The ADP coding sequence may be used as G1 or
XX G2. (A) has greater specificity for a target cell than a similar vector
XX in which TRE is operably linked to a gene and which lacks an IRES. (A)
XX are used to modify the genotype of target cells, optionally in vitro with
XX subsequent return of altered cells to the host and where G2 is a
XX cytotoxic gene, to confer selective cytotoxicity to target cells,
XX especially for killing cancer cells. ADP displays a cytotoxic,
XX particularly cell lysis, function. Also (A) are used for diagnosis and
XX monitoring, e.g. detection of bladder cancer cells. The target cell-
XX specific TRE ensures that (A) has better targeting specificity, with
XX minimal replication in non-target cells, so a runaway infection is
XX prevented but production of adenoviral proteins in target cells activates
XX and/or stimulates the immune response against target cells producing such
XX proteins. The use of an IRES (rather than two identical control elements)
XX eliminates the risk of homologous recombination and may provide enough
XX extra space for an additional (therapeutic) gene. (Updated on 11-SEP-2003
XX to standardise OS field)
XX Sequence 101 AA;
Query Match 100.0%; Score 551; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-61;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
QY 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101
DB 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101
RESULT 9
ABG69353
ID ABG69353 standard; protein; 101 AA.
XX AC ABG69353;
XX AC ABG69353;
XX 21-OCT-2002 (first entry)
XX Adenovirus death protein (ADP).
XX Adenovirus; transcriptional regulatory element; TRE; prostate; liver;
XX breast cancer; colon cancer; antitumour; adenovirus death protein.
XX

OS Unidentified.
XX US2002068049-A1.
XX 06-JUN-2002.
XX 06-DEC-2000; 2000US-00732169.
XX 10-SEP-1998; 98US-00151376.
XX (HEND/) HENDERSON D R.
XX (SCHU/) SCHUUR E R.
XX Henderson DR, Schuur ER;
XX WPI; 2002-582468/62.
XX N-PSDB; ABK99587.
XX Novel adenovirus vector comprises adenovirus gene under transcriptional
XX control of cell-type specific transcriptional response element for
XX conferring selective toxicity on target cell and for suppressing tumor
XX growth.
XX Disclosure; Fig 19; 83pp; English.
XX The invention relates to an adenovirus vector (AV) comprising an AV gene
XX under transcriptional control of a cell type-specific transcriptional
XX regulatory element (TRE) and optionally a first AV gene under control of
XX a first cell type-specific TRE and a second gene under control of a
XX second cell type-specific TRE, where the first and second cell type-
XX specific TREs are substantially identical. When the vector is introduced
XX into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon
XX cancer cell) it allows the cell type-specific TRE to function, resulting
XX in cytotoxicity. The vector is useful for suppressing tumour growth of a
XX target cell. This sequence represents a polypeptide used in the scope of
XX the invention
XX Sequence 101 AA;
Query Match 100.0%; Score 551; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-61;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
QY 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101
DB 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101
RESULT 10
ABU10308
ID ABU10308 standard; protein; 101 AA.
XX AC ABU10308;
XX AC ABU10308;
XX 23-OCT-2003 (revised)
XX 07-AUG-2003 (first entry)
XX Adenovirus death protein (ADP).
XX Adenoviral vector; adenovirus gene; transcriptional control; TRE;
XX cell type-specific; transcriptional response element; PSA; hKLK;
XX prostate-specific antigen; glandular kallikrein; probastin; PS;
XX carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1;
XX cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic;
XX adenovirus death protein; ADP.
XX unidentifed adenovirus.
XX US2003044383-A1.
PN

```

XX 06-MAR-2003.
XX
XX 10-SEP-1998; 98US-00151376.
XX
XX 27-JUN-1995; 95US-00495034.
XX 20-AUG-1996; 96US-00699753.
XX 03-MAR-1997; 97US-0039597P.
XX 03-MAR-1997; 97US-0039599P.
XX 03-MAR-1997; 97US-0039762P.
XX 03-MAR-1997; 97US-0039763P.
XX 02-MAR-1998; 98US-00033333.
XX 02-MAR-1998; 98US-00033428.
XX 02-MAR-1998; 98US-00033555.
XX (HEND/) HENDERSON D R.
XX (SCHU/) SCHUUR E R.
XX
XX Henderson DR, Schuur ER;
XX
XX WPI; 2003-456547/43.
XX N-PSDB; ACD07312.
XX
XX New adenovirus vector for transfecting target host cells, comprises an
XX adenovirus gene under transcriptional control of a cell type-specific
XX transcriptional response element.
XX
XX Disclosure; Fig 19; 83pp; English.
XX
XX The present invention relates to adenoviral vectors comprising an
XX adenovirus gene under transcriptional control of a cell type-specific
XX transcriptional response element (TRE). Example TREs given in the
XX specification include human prostate-specific antigen (PSA) TRE, human
XX glandular kallikrein (hKLK) TRE, rat probastin (PB) TRE, human
XX carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3
XX (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for
XX introducing new genetic capability, particularly associated with
XX cytotoxicity for treating neoplasia. For example, the vector may be used
XX in a target cell to suppress tumour growth, or to kill the target cell.
XX The vector is particularly useful in gene therapy. The present sequence
XX represents adenovirus death protein (ADP). (Updated on 23-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 101 AA;
XX
XX Query Match 100.0%; Score 551; DB 6; Length 101;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-61;
XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
XX
XX 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
XX
XX 61 CLKRRRARPPPIYRPIIVLNPNEKIHRLDGLKPCSLLLQYD 101
XX
XX 61 CLKRRRARPPPIYRPIIVLNPNEKIHRLDGLKPCSLLLQYD 101
XX
XX RESULT 11
XX ADI36347
XX ID ADI36347 standard; protein; 101 AA.
XX AC ADI36347;
XX
XX 22-APR-2004 (first entry)
XX
XX Human ADP protein sequence SeqID 11.
XX
XX human; prostate; transcriptional response element; TRE;
XX polyethylene glycol; PEG; masking agent; tumour cell growth;
XX proliferation; psoriatic lesion; wound healing; hyperplasia; cancer;
XX cytostatic; antipsoriatic; vulnery; ADP.
XX
XX
XX Homo sapiens.
XX
XX US2003152553-A1.
XX
XX 14-AUG-2003.
XX
XX 02-MAY-2002; 2002US-00139089.
XX
XX 27-JUN-1995; 95US-00495034.
XX 26-JUN-1996; 96US-00669753.
XX 03-MAR-1997; 97US-0039597P.
XX 03-MAR-1997; 97US-0039762P.
XX 03-MAR-1997; 97US-0039763P.
XX 02-MAR-1998; 98US-00033333.
XX 02-MAR-1998; 98US-00033428.
XX 02-MAR-1998; 98US-00033555.
XX 10-SEP-1998; 98US-00151376.
XX 02-JUN-2000; 2000US-00509591.
XX
XX (LITT/) LITTLE A S.
XX (LAME/) LAMPARSKI H G.
XX (HEND/) HENDERSON D R.
XX (SCHU/) SCHUUR E R.
XX
XX Little AS, Lamparski HG, Henderson DR, Schuur ER;
XX
XX WPI; 2004-119002/12.
XX N-PSDB; ADI36417.
XX
XX Composition comprising replication competent adenovirus having adenovirus
XX gene essential for replication under transcriptional control of cell type
XX specific transcriptional response element and masking agent.
XX
XX Disclosure; SEQ ID NO 11; 115pp; English.
XX
XX This invention relates to a novel composition that contains a replication
XX competent adenovirus capable of transfecting target host cells.
XX Specifically, it comprises an adenoviral gene essential for replication
XX (E1A, E1B or E4), which is under the transcriptional control of a
XX prostate specific transcriptional response element (TRE) and polyethylene
XX glycol (PEG) as the masking agent. The present invention describes this
XX composition as useful for suppressing tumour cell growth and for lowering
XX the levels of tumour cell markers. It can also be used for introducing
XX transient expression other than tumours, such as psoriatic lesions and wound
XX healing. In addition, it is useful for detecting cells where a cell type-
XX specific TRE is functional in a biological sample and for treating
XX prostate-associated diseases such as hyperplasia and cancer. As such,
XX these compositions exhibit cytostatic, antipsoriatic and vulnery
XX activities. This polypeptide sequence is the human ADP protein of the
XX invention.
XX
XX Sequence 101 AA;
XX
XX Query Match 100.0%; Score 551; DB 8; Length 101;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-61;
XX Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
XX
XX 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
XX
XX 61 CLKRRRARPPPIYRPIIVLNPNEKIHRLDGLKPCSLLLQYD 101
XX
XX 61 CLKRRRARPPPIYRPIIVLNPNEKIHRLDGLKPCSLLLQYD 101
XX
XX RESULT 12
XX ADV20979
XX ID ADV20979 standard; protein; 101 AA.
XX XX ADV20979;
XX XX

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DT 24-FEB-2005 (first entry)
 DE Adenovirus death protein (ADP).
 XX
 XX
 KW Vector; gene transfer; cloning vehicle; genetic engineering;
 KW prostate cancer; gene therapy; vaccine; cytostatic;
 KW prostate-specific antigen; TRE; transcriptional regulatory element; PSE;
 KW prostate specific enhancer; PSA; prostate specific antigen; cancer;
 KW adenovirus death protein; ADP.
 XX
 OS unidentified adenovirus.
 XX
 XX US2004241857-A1.
 PN
 XX 02-DEC-2004.
 PD
 XX
 XX 13-APR-2004; 2004US-00822873.
 XX
 XX 27-JUN-1995; 95US-00495034.
 PR 26-JUN-1996; 96US-00669753.
 PR 10-SEP-1998; 98US-00151376.
 PR 06-DEC-2000; 2000US-00732169.
 XX
 XX (HEND/) HENDERSON D R.
 PA (SCHU/) SCHUUR E R.
 PA
 XX
 XX Henderson DR, Schuur ER;
 PI
 XX WPI; 2005-011642/01.
 DR
 XX New adenovirus vector comprising an adenovirus early gene essential for
 PT propagation under the control of a human prostate specific antigen
 PT promoter and a human prostate specific antigen enhancer, for treating
 PT prostate cancer.
 PT
 XX
 PS Disclosure; SEQ ID NO 11; 112pp; English.
 XX
 CC The present invention relates to an adenovirus vector comprising an
 CC adenovirus early gene essential for propagation under the control of a
 CC human prostate specific antigen promoter and a human prostate specific
 CC antigen (PSA) enhancer. The invention is useful for treating a patient
 CC suffering from prostate cancer and for making mammalian hosts that are
 CC transiently transgenic and for detecting the presence of cells that
 CC permit the function of a cell type-specific transcriptional regulatory
 CC element (TRE) in a sample. The invention is also used in the gene therapy
 CC and also as vaccine. The present sequence is the adenovirus death protein
 CC (ADP).
 XX
 SQ Sequence 101 AA;
 Query Match 100.0%; Score 551; DB 9; Length 101;
 Best Local Similarity 100.0%; Pred. No. 2.5e-61;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
 DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
 QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
 DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
 RESULT 13
 ADW47775
 ID ADW47775 standard; protein; 101 AA.
 XX
 AC ADW47775;
 XX
 XX 07-APR-2005 (first entry)
 DT Adenovirus death protein.
 XX
 XX
 KW Gene therapy; vector; prostate tumor; cytostatic; vasotropic; vulnery;
 KW antipsoriatic; antimicrobial; immunomodulator.
 OS Human adenovirus type 2.
 PN WO2005007832-A2.
 XX
 PD 27-JAN-2005.
 XX
 XX 24-FEB-2004; 2004WO-US005518.
 XX
 XX 24-FEB-2003; 2003US-0450232P.
 PR
 XX (CELL-) CELL GENESYS INC.
 PA
 XX
 XX Harding T, Yu DC;
 PI
 XX WPI; 2005-102098/11.
 DR N-PSDB; ADW47774.
 DR
 XX New replication competent adenovirus vector comprising an inducible
 PT transcriptional transactivator coding sequence and an adenovirus gene,
 PT useful for treating cancer, psoriatic lesions, restenosis or wound
 PT healing.
 PT
 XX
 PS Disclosure; SEQ ID NO 11; 66pp; English.
 XX
 CC The present sequence is the protein sequence of adenovirus death protein
 CC (ADP). A claimed replication competent adenovirus vector comprises: an
 CC inducible transcriptional transactivator (TT) coding sequence under the
 CC transcriptional control of a cell type-specific TRE (CT-TRE); and an
 CC adenovirus gene under transcriptional control of a TRE regulated by the
 CC TT, where the TT is functionally responsive to an exogenous inducer
 CC agent. The adenovirus gene is preferably a gene essential for adenoviral
 CC replication. The TT may be inhibited or activated by the inducing agent.
 CC Also claimed is an adenovirus vector comprising: an inducible TT coding
 CC sequence under the transcriptional control of a CT-TRE; and an adenovirus
 CC gene under transcriptional control of a TRE regulated by the TT and a
 CC second gene under transcriptional control of a second TRE, where the TT
 CC is activated by an exogenous inducing agent. The second gene may an
 CC adenoviral gene essential for adenovirus replication, or a transgene such
 CC as a cytotoxic gene. One embodiment of the invention provides adenovirus
 CC vectors in which an adenovirus gene is under transcriptional control of a
 CC first transactivated regulated TRE and a polynucleotide encoding an ADP
 CC under control of a second transactivator regulated TRE, where the
 CC adenovirus gene is essential for replication. Also claimed are host cells
 CC comprising the replication competent adenovirus vector, and methods for
 CC propagating and regulating the vector. A claimed method for selective
 CC cytolysis of a target tumor cell line involves introducing the adenovirus
 CC vector into a cell which allows the CT-TRE to function, and administering
 CC an inducing agent such that the adenovirus vector is propagated and
 CC causes lysis of target prostate cells. The adenovirus vector can also be
 CC used to treat psoriatic lesions, restenosis, wound healing, tissue
 CC repair, enhanced immune response, resistance to infection, production of
 CC factors, enhanced proliferation, investigation of metabolic or other
 CC physiological pathways, or comparison of activity of cells in the
 CC presence and absence of the virus introduced transgene. In vectors of the
 CC invention, expression of a viral gene essential for replication is
 CC regulated both by the CT-TRE and the transactivator regulated TRE, and
 CC indirectly by the concentration of the inducing agent.
 XX
 SQ Sequence 101 AA;
 Query Match 100.0%; Score 551; DB 9; Length 101;
 Best Local Similarity 100.0%; Pred. No. 2.5e-61;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
 DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
 QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
 DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

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Db 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101
RESULT 14
AAW59925
ID AAW59925 standard; protein; 101 AA.
XX AC AAW59925;
XX DT 11-JAN-1999 (first entry)
XX DE Adenovirus death protein.
XX KW Adenovirus death protein; ADP; transcription regulatory element; vector;
XX KW breast cancer; prostate cancer; liver cancer; colon cancer; gene therapy.
XX OS Mastadenovirus.
XX PN WO9839464-A2.
XX PD 11-SEP-1998.
XX PF 03-MAR-1998; 98WO-US004080.
XX PR 03-MAR-1997; 97US-0039762P.
XX PR 03-MAR-1997; 97US-0039763P.
XX PR 04-AUG-1997; 97US-0054523P.
XX PR 02-MAR-1998; 98US-00033556.
XX PA (CALY-) CALYDON INC.
XX PI Henderson DR, Yu D, Lamparski HG;
XX DR WPI; 1998-495860/42.
XX DR N-PSDB; AAV53632.
XX PT New adenovirus vectors, used for treating tumours - comprising first and
XX PT second adenovirus genes under control of different heterologous
XX PT transcriptional regulatory elements.
XX PS Disclosure; Page 94; 130pp; English.
XX CC This is the amino acid sequence of adenovirus death protein (ADP). The
XX CC invention provides replication-competent adenovirus vectors specific for
XX CC target cells and methods of using such vectors. The vectors contain
XX CC heterologous transcription regulatory elements (TREs) and may incorporate
XX CC a gene, such as the ADP gene (see AAV53632), which can contribute to
XX CC cytotoxicity in the target cell. Adenoviral replication can be restricted
XX CC to target cells in which the heterologous TREs are functional and thus
XX CC the vectors can provide selective cytotoxicity to the target cells (e.g.
XX CC prostate, liver, breast or colon), particularly neoplastic cells
XX SQ Sequence 101 AA;
Query Match 99.3%; Score 547; DB 2; Length 101;
Best Local Similarity 99.0%; Pred. No. 7.9e-61;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTGSTIAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTIAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101
DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101
RESULT 15
ADW28321
ID ADW28321 standard; protein; 101 AA.
XX AC ADW28321;
XX
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```
DT 07-APR-2005 (first entry)
XX Amino acid sequence of adenovirus type 5 adenovirus death protein.
DE Chemotherapy; cytosine deaminase; thymidine kinase; death protein;
XX cancer; neoplaam; 5-fluorocytosine; ganciclovir.
KW Human adenovirus type 5.
XX OS
XX PH Key Location/Qualifiers
FT Misc-difference 63 /note= "Ala encoded by AAG"
XX FT
XX WO2005007109-A2.
XX PN 27-JAN-2005.
XX PD
XX PF 09-JUL-2004; 2004WO-US022320.
XX PR 09-JUL-2003; 2003US-0486219P.
XX PA (FORD-) FORD HEALTH SYSTEM HENRY.
XX PI Freytag SD, Kim JH, Barton K, Paielli D;
XX DR WPI; 2005-101983/11.
XX DR N-PSDB; ADW28319.
XX PT Novel isolated polynucleotide comprising nucleotide sequence of yeast
XX PT cytosine deaminase/mutant SR 39 herpes simplex virus type 1 thymidine
XX PT kinase fusion gene, useful for treating mammalian patient having
XX PT malignancy or solid tumor.
XX PS Example; Page 54; 62pp; English.
XX CC The specification describes a polynucleotide comprising a nucleotide
XX CC sequence of yeast cytosine deaminase/mutant SR39 herpes simplex virus
XX CC type 1 thymidine kinase fusion gene, and further comprising an adenovirus
XX CC type 5 adenovirus death protein gene. The polynucleotide of the invention
XX CC limits the side effects of cancer treatment by using only lower doses of
XX CC radiation. The polypeptide encoded by the above polynucleotide is useful
XX CC for converting 5-fluorocytosine or ganciclovir into active
XX CC chemotherapeutic agents. Pharmaceutical compositions comprising
XX CC recombinant adenoviruses comprising polynucleotides of the invention are
XX CC useful for treating a mammalian patient having a malignancy or solid
XX CC tumor. The present sequence represents an adenovirus type 5 adenovirus
XX CC death protein, which is used to construct polynucleotides of the
XX CC invention.
XX SQ Sequence 101 AA;
Query Match 98.9%; Score 545; DB 9; Length 101;
Best Local Similarity 99.0%; Pred. No. 1.4e-60;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTGSTIAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTIAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101
DB 61 CLARRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101
Search completed: January 18, 2006, 19:46:33
Job time : 79 secs
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:29:41 ; Search time 391 Seconds
(without alignments)
647.192 Million cell updates/sec

Title: US-10-822-873-10

Perfect score: 307

Sequence: 1 gatgacggctcaaccatcg.....ttctttacagatgattaa 307

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6049916 seqs, 412136615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.New.*

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4: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq.*
5: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq.*
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9: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq2.*
10: /cgn2_6/prodata/1/pubpna/US11_NEW_PUB.seq3.*
11: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	35937	US-11-127-832-3	Sequence 3, Appli
2	196	63.8	35696	US-10-860-436-1	Sequence 1, Appli
3	196	63.8	35893	US-10-860-436-2	Sequence 2, Appli
4	196	63.8	35935	US-11-127-832-4	Sequence 4, Appli
5	196	63.8	35935	US-11-127-832-5	Sequence 5, Appli
6	145	47.2	1172	US-11-066-480-5	Sequence 4, Appli
C 7	35.6	11.6	191350	US-10-857-780-4	Sequence 3556, Ap
C 8	33.2	10.8	2926	US-11-136-527-3556	Sequence 49060, A
9	31.2	10.2	872	US-10-750-185-49060	Sequence 49060, A
10	31.2	10.2	872	US-10-750-623-49060	Sequence 49060, A
11	31	10.1	1542	US-10-750-185-47255	Sequence 47255, A
12	31	10.1	1542	US-10-750-623-47255	Sequence 47255, A
13	30.6	10.0	1009	US-11-136-527-4007	Sequence 4007, Ap
14	30.6	10.0	1009	US-11-136-527-8103	Sequence 8103, Ap
15	30.2	9.8	1691140	US-11-091-018-1	Sequence 1, Appli
C 16	29.4	9.6	928	US-10-750-185-59931	Sequence 59931, A
C 17	29.4	9.6	928	US-10-750-623-59931	Sequence 59931, A
C 18	29.2	9.5	567	US-11-052-554A-575	Sequence 575, App
C 19	29.2	9.5	2563	US-10-750-185-53160	Sequence 53160, A
C 20	29.2	9.5	2563	US-10-750-623-53160	Sequence 53160, A
C 21	29.2	9.5	3486	US-10-750-185-42580	Sequence 42580, A
C 22	29.2	9.5	3486	US-10-750-623-42580	Sequence 42580, A

ALIGNMENTS

RESULT 1

US-11-127-832-3
; Sequence 3, Application US/11127832
; Publication No. US2006000884A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/11/127,832
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/09/782,378
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 35937
; TYPE: DNA
; ORGANISM: Human adeno-associated virus 2
US-11-127-832-3

Query Match	100.0%	Score 307;	DB 8;	Length 35937;
Best Local Similarity	100.0%;	Pred. No. 1.9e-96;		
Matches 307;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GATGACGGCTCAACCATCGCGCCCAACAGCACTATCGCAACCACTGCTACCGGACT	60	
Db	29467	GATGACGGCTCAACCATCGCGCCCAACAGCACTATCGCAACCACTGCTACCGGACT	29526	
QY	61	AACATCTGCGCTTAAATTTACCCCAAGTTTCATCGCTTTGTCAATGACTGGCGAGCTTGGGA	120	
Db	29527	AACATCTGCGCTTAAATTTACCCCAAGTTTCATCGCTTTGTCAATGACTGGCGAGCTTGGGA	29586	
QY	121	CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATATATGTCGCTTATTTG	180	
Db	29587	CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATATATGTCGCTTATTTG	29646	
QY	181	TTGCTCTAAAGCCGACAGCGCCAGACCCCGCTATATAGCCCTCATTTGTGCTCAACCC	240	
Db	29647	TTGCTCTAAAGCCGACAGCGCCAGACCCCGCTATATAGCCCTCATTTGTGCTCAACCC	29706	

Qy	241	ACACAATGAAAAAATTTCATAGATTGGACCGTCTGAAACCATGTTCTCTCTCTCTTTACAGTA	300
Db	29707	ACACAATGAAAAAATTTCATAGATTGGACCGTCTGAAACCATGTTCTCTCTCTTTTACAGTA	29766
Qy	301	TGATTAA	307
Db	29767	TGATTAA	29773

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RESULT 2
US-10-860-436-1
  ? Sequence 1, Application US/10860436
  ? Publication No. US20050271622A1
  ? GENERAL INFORMATION:
  ? APPLICANT: Zhou, Jiansheng
  ? APPLICANT: Ma, Ding
  ? APPLICANT: Lu, Yunping
  ? APPLICANT: Wang, Shixuan
  ? APPLICANT: Chen, Gang
  ? APPLICANT: Gao, Ginglei
  ? TITLE OF INVENTION: CONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT
  ? TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
  ? TITLE OF INVENTION: AND USES THEREOF
  ? FILE REFERENCE: 850141.402
  ? CURRENT APPLICATION NUMBER: US/10/860,436
  ? CURRENT FILING DATE: 2004-06-03
  ? NUMBER OF SEQ ID NOS: 15
  ? *SOFTWARE: FastSeq for Windows Version 4.0
  ? SEQ ID NO 1
  ? LENGTH: 35696
  ? TYPE: DNA
  ? ORGANISM: Artificial Sequence
  ? FEATURE:
  ? OTHER INFORMATION: recombinant adenovirus delta920-946ADV5/ASCH6
US-10-860-436-1

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Query Match	63.8%	Score 196;	DB 7;	Length 35696;
Best Local Similarity	86.4%;	Pred. No. 1.2e-57;		
Matches 228;	Conservative	0;	Mismatches 35;	Indels 1; Gaps 1;
Qy	45	CCACTGCTACCGGACTAAACATCTGCCTCTAAATTTACCCCAAGTTCATGCGCTTTGTCAATG	104	
Db	29274	CCGCGCTACCGGACTTACATCTACCACAAATACACCCCAAGTTCTGCCTTTGTCAATA	29333	
Qy	105	ACTGGGCGAGCTTGGACATCTGGTGGTTTTCCATAGCGCTTATGTTTGTTCGCTTATTA	164	
Db	29334	ACTGGGATACTTGGGATGTGGTGGTTCTCCATAGCGCTTATGTTTGTATGCCTTATTA	29393	
Qy	165	TTATGTGGCTTATTTGTGTGCTTAAACGCGACGCGCCAGACCCGCCCATCTATAGGCCTA	224	
Db	29394	TTATGTGGCTCATCTGTGCTTAAAGCGCAACCGCGCCCGACACCCCATCTATAGTCCCA	29453	
Qy	225	TCATTGTGCTCAACCCACACAAATGAAAATTTATAGATTGGACGGTCTGGAAC-CATGT	283	
Db	29454	TCATTGTGCTACACCCCAACAAATGATGGAATCCATAGATTGGACGGGACTGAAACACATGT	29513	
Qy	284	TCCTCTCTTTTACAGTATGATTAA	307	
Db	29514	TCCTTTCTCTTACAGTATGATTAA	29537	

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RESULT 3
US-10-860-436-2
; Sequence 2, Application US/10860436
; Publication No. US20050271622A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Jianfeng
; APPLICANT: Ma, Ding
; APPLICANT: Lu, Yumping
; APPLICANT: Wang, Shixuan
; APPLICANT: Chen, Gang
; APPLICANT: Gao, Ginglei
; TITLE OF INVENTION: CONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT

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; TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 850141.402
; CURRENT APPLICATION NUMBER: US/10/860,436
; CURRENT FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 35893
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recombinant adenovirus delta920-946ADV5/ASPLK1
; US-10-860-436-2

Query Match      63.8%; Score 196; DB 7; Length 35893;
Best Local Similarity 86.4%; Pred. No. 1.2e-57;
Matches 228; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

Qy 45 CCACGCTACCGGACTTAACATCTGCGCCCTAAATTTACCCCAAGTTTCATGCCCTTTGTCAATG 104
Db 29471 CGCGCGCTACCGGACTTACATCTACCAAAATACACCCCAAGTTTCTGCCCTTTGTCAATA 29530

Qy 105 ACTGGCGCAGCTTGGACATGTGGTGGTGTTCATATGCGCTTATGTTGTTCCTTATTA 164
Db 29531 ACTGGGATAACTTGGGCATGTGGTGGTCTCCATAGCGCTTATGTTGTATGCGCTTATTA 29590

Qy 165 TTATGTGGCTTATTTGTTGGCTTAAGCCGAGCGGCCAGACCCCACTATAGGCCTA 224
Db 29591 TTATGTGGCTCATCTGCTGGCTTAAAGCGCAACGCGCCGACCCCACTATAGTCCTCA 29650

Qy 225 TCATTGTGCTCAACCCACCAACATGAAAAAATTTCATAGATTGGACGGTCTGAAAC-CATGT 283
Db 29651 TCATTGTGCTACACCAACAAATGATGGATCCATAGATTGGACGGACTGAAACACATGT 29710

Qy 284 TCCTCTCTTTTACGATGATGATTA 307
Db 29711 TCCTTCTCTTACGATGATGATTA 29734

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RESULT 4
US-11-127-832-4
; Sequence 4, Application US/11127832
; Publication No. US2006000884A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/11/127,832
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/09/782,378
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Human adenovirus type 5
US-11-127-832-4

```

APPLICANTS: GAO, GUIGUET
TITLE OF INVENTION: CONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT

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QY 105 ACTGGCGAGCTTGGACATGTGGTGGTTTCCATAGCGCTTATGTTTGTGCTTATTA 164
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29573 ACTGGGTAACCTTGGGCATGTGGTGGTCTCCATAGCGCTTATGTTTGTGCTTATTA 29632

QY 165 TTATGGGCTTATTTGTTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCCTA 224
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29633 TTATGGGCTCATCTGCTGCTTAAAGCGCAACGCGCCGACCATCTATAGTCCCA 29692

QY 225 TCATTGGCTCAACCCACACATGAAAAATTCATAGATTGGAGCGTCTGAAC-CATGT 283
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 29693 TCATTGGCTACACCCCAACATGGAATCCATAGATTGGAGCGTGAACACATGT 29752

QY 284 TCCTCTCTTTTACAGTATGATTAA 307
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Db 29753 TCCTCTCTTACAGTATGATTAA 29776

RESULT 5
US-11-127-832-5
; Sequence 5, Application US/11127832
; Publication No. US2006008884A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/11/127,832
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/09/782,378
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Human adenovirus type 5
US-11-127-832-5

Query Match 63.8%; Score 196; DB 8; Length 35935;
Best Local Similarity 86.4%; Pred. No. 1.2e-57;
Matches 228; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 45 CCACTGCTACCGACTTAACATCTGCCCTAAATTTACCCCAAGTTTCATGCCCTTTGTCAATG 104
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Db 29513 CCGCGCTACCGACTTACATCTACCAATAACACCCCAAGTTTCTGCCCTTTGTCAATA 29572

QY 105 ACTGGCGAGCTTGGACATGTGGTGGTTTCCATAGCGCTTATGTTTGTGCTTATTA 164
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Db 29573 ACTGGGTAACCTTGGGCATGTGGTGGTCTCCATAGCGCTTATGTTTGTGCTTATTA 29632

QY 165 TTATGGGCTTATTTGTTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCCTA 224
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Db 29633 TTATGGGCTCATCTGCTGCTTAAAGCGCAACGCGCCGACCATCTATAGTCCCA 29692

QY 225 TCATTGGCTCAACCCACACATGAAAAATTCATAGATTGGAGCGTCTGAAC-CATGT 283
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Db 29693 TCATTGGCTACACCCCAACATGGAATCCATAGATTGGAGCGTGAACACATGT 29752

QY 284 TCCTCTCTTTTACAGTATGATTAA 307
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Db 29753 TCCTCTCTTACAGTATGATTAA 29776
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RESULT 6
US-11-066-480-5
; Sequence 5, Application US/11066480
; Publication No. US2005028280A1
; GENERAL INFORMATION:
; APPLICANT: ENNIST, DAVID LEONARD
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; TITLE OF INVENTION: ONCOLYTIC ADENOVIRAL ENCODING GM-CSF
; FILE REFERENCE: GTIN-001
; CURRENT APPLICATION NUMBER: US/11/066,480
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/10/925,205
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: 60/499,312
; PRIOR FILING DATE: 2003-08-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1172
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: 28781 to 29952 of Ar20-1007 including the E3-6.7 gene, and the hu
US-11-066-480-5

Query Match 47.2%; Score 145; DB 8; Length 1172;
Best Local Similarity 86.5%; Pred. No. 1.1e-40;
Matches 160; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 45 CCACTGCTACCGACTTAACATCTGCCCTAAATTTACCCCAAGTTTCATGCCCTTTGTCAATG 104
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 988 CCGCGCTACCGACTTACATCTACCAATAACACCCCAAGTTTCTGCCCTTTGTCAATA 1047

QY 105 ACTGGCGAGCTTGGACATGTGGTGGTTTCCATAGCGCTTATGTTTGTGCTTATTA 164
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1048 ACTGGGTAACCTTGGGCATGTGGTGGTCTCCATAGCGCTTATGTTTGTGCTTATTA 1107

QY 165 TTATGGGCTTATTTGTTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCCTA 224
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Db 1108 TTATGGGCTCATCTGCTGCTTAAAGCGCAACGCGCCGACCATCTATAGTCCCA 1167

QY 225 TCATT 229
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Db 1168 TCATT 1172

RESULT 7
US-10-857-780-4/c
; Sequence 4, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: RENELAND, RIKARD HENRY
; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 191350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16914)..(16914)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
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; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49060
; LENGTH: 872
; TYPE: DNA
; ORGANISM: Bovine 19866881284640
; US-10-750-623-49060

Query Match      10.2%; Score 31.2; DB 7; Length 872;
Best Local Similarity 55.6%; Pred. No. 0.85; Indels 0; Gaps 0;
Matches 60; Conservative 0; Mismatches 48;

QY 81 CCCAAGTTCATGCTTTGTCAATGACTGGCGAGCTTGGACATGTGGTGTTCATAG 140
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Db 591 CCAAGAGCCTGCCAGCAGACAGTCAGGTTCAGCCTGTAGTCTGTGTGTTCTGG 650

QY 141 CGCTTATGTTTGGCTTATTATTAATGATGAGTGTATTTGTCCTAA 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 651 TGCATATCAAGGATGCTATTTTTCATCTCTCTACCATGTTGCCAA 698

RESULT 11
US-10-750-185-47255
; Sequence 47255, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47255
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Bovine 19866880533767
; US-10-750-185-47255

Query Match      10.1%; Score 31; DB 7; Length 1542;
Best Local Similarity 49.7%; Pred. No. 1.3;
Matches 79; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 144 TTATGTTTGGCTTATTATTTATGTCGCTTATTTGTCCTAAAGCGCAGCGCCA 203
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Db 370 TTAAGAGTGTTCATGATAAATAATTTGTGCATATTTGCTGTTGTCCTCTGTGTC 429

QY 204 GACCCCATCTATAGCCCTATCATTTGCTCAACCCACACAAATGAAATTCATAGAT 263
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Db 430 CATCCATCTTTAAAAAATAATTTGCTGTAATCTTGAAGTGAATTCATATATCA 489

RESULT 12
US-10-750-623-47255
; Sequence 47255, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47255
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Bovine 19866880533767
; US-10-750-623-47255

Query Match      10.1%; Score 31; DB 7; Length 1542;
Best Local Similarity 49.7%; Pred. No. 1.3;
Matches 79; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 144 TTATGTTTGGCTTATTATTTATGTCGCTTATTTGTCCTAAAGCGCAGCGCCA 203
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Db 370 TTAAGAGTGTTCATGATAAATAATTTGTGCATATTTGCTGTTGTCCTCTGTGTC 429

QY 204 GACCCCATCTATAGCCCTATCATTTGCTCAACCCACACAAATGAAATTCATAGAT 263
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Db 430 CATCCATCTTTAAAAAATAATTTGCTGTAATCTTGAAGTGAATTCATATATCA 489

RESULT 13
US-11-136-527-4007
; Sequence 4007, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4007
; LENGTH: 1009
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-4007

Query Match      10.0%; Score 30.6; DB 8; Length 1009;
Best Local Similarity 47.2%; Pred. No. 1.5;
Matches 93; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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QY 264 TGGACGGTCTGAAACCATGTTCTCTCTCTTTTACAGTATG 302
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Db 490 TGATACTCTTAGAGTGTCACTTTTGTGTTAAGAGTG 528

RESULT 12
US-10-750-623-47255
; Sequence 47255, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47255
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Bovine 19866880533767
; US-10-750-623-47255

Query Match      10.1%; Score 31; DB 7; Length 1542;
Best Local Similarity 49.7%; Pred. No. 1.3;
Matches 79; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 144 TTATGTTTGGCTTATTATTTATGTCGCTTATTTGTCCTAAAGCGCAGCGCCA 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 370 TTAAGAGTGTTCATGATAAATAATTTGTGCATATTTGCTGTTGTCCTCTGTGTC 429

QY 204 GACCCCATCTATAGCCCTATCATTTGCTCAACCCACACAAATGAAATTCATAGAT 263
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 CATCCATCTTTAAAAAATAATTTGCTGTAATCTTGAAGTGAATTCATATATCA 489

RESULT 13
US-11-136-527-4007
; Sequence 4007, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4007
; LENGTH: 1009
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-4007

Query Match      10.0%; Score 30.6; DB 8; Length 1009;
Best Local Similarity 47.2%; Pred. No. 1.5;
Matches 93; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:21:44 ; Search time 803 Seconds
(without alignments)
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Title: US-10-822-873-10

Perfect score: 307

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published Applications NA_Main:

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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	307	3	US-09-392-822-8
2	307	100.0	307	3	US-09-814-292-3
3	307	100.0	307	3	US-09-875-228-4
4	307	100.0	307	3	US-09-998-883-22
5	307	100.0	307	3	US-09-151-376-10
6	307	100.0	307	3	US-09-151-376-61
7	307	100.0	307	3	US-09-814-357-17
8	307	100.0	307	3	US-09-814-351-17
9	307	100.0	307	5	US-10-045-116-19
10	307	100.0	307	5	US-10-222-479-21
11	307	100.0	307	6	US-10-139-089-10
12	307	100.0	307	6	US-10-139-089-61
13	307	100.0	307	7	US-10-691-045-17
14	307	100.0	307	8	US-10-822-873-10
15	307	100.0	307	8	US-10-822-873-61
16	307	100.0	307	9	US-10-938-227-7
17	307	100.0	34616	7	US-10-384-136-2
18	307	100.0	35937	3	US-09-782-378A-3
19	307	100.0	35937	9	US-10-794-514A-731
20	303.8	99.0	34427	3	US-09-111-911-5
21	302.2	98.4	35759	8	US-10-645-883A-9
22	196	63.8	34541	8	US-10-859-739-15
23	196	63.8	35408	5	US-10-155-649-3

24	196	63.8	35712	9	US-10-860-630-1	Sequence 1, Appli
25	196	63.8	35871	3	US-09-956-335-2	Sequence 2, Appli
26	196	63.8	35909	3	US-10-860-630-2	Sequence 2, Appli
27	196	63.8	35935	3	US-09-725-720-43	Sequence 43, Appli
28	196	63.8	35935	3	US-09-782-378A-4	Sequence 4, Appli
29	196	63.8	35935	3	US-09-782-378A-5	Sequence 5, Appli
30	196	63.8	35935	3	US-09-739-007-43	Sequence 43, Appli
31	196	63.8	35935	7	US-10-264-839-12	Sequence 12, Appli
32	196	63.8	35935	7	US-10-432-989-1	Sequence 1, Appli
33	196	63.8	35935	7	US-10-433-681-1	Sequence 1, Appli
34	196	63.8	35935	8	US-10-766-307A-4	Sequence 4, Appli
35	196	63.8	35935	8	US-10-492-178-8	Sequence 8, Appli
36	196	63.8	35935	8	US-10-492-178-9	Sequence 9, Appli
37	196	63.8	35935	9	US-10-612-285-1	Sequence 1, Appli
38	196	63.8	35938	9	US-10-794-514A-732	Sequence 732, App
39	196	63.8	35978	3	US-09-956-335-1	Sequence 1, Appli
40	196	63.8	36083	9	US-10-944-496-21	Sequence 21, Appli
41	196	63.8	36620	3	US-09-952-060-30	Sequence 30, Appli
42	196	63.8	36620	7	US-10-380-641-30	Sequence 30, Appli
43	196	63.8	36620	9	US-10-636-730-30	Sequence 30, Appli
44	196	63.8	37474	3	US-09-952-060-25	Sequence 25, Appli
45	196	63.8	37474	7	US-10-380-641-25	Sequence 25, Appli

ALIGNMENTS

RESULT 1

US-09-392-822-8
; Sequence 8, Application US/09392822
; Patent No. US20010053352A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: Adenovirus Vectors Containing Cell
; TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
; FILE REFERENCE: 348022001200
; CURRENT APPLICATION NUMBER: US/09/392,822
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: 60/099,791
; EARLIER FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Adenovirus V
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(304)
US-09-392-822-8

Query Match 100.0%; Score 307; DB 3; Length 307;					
Best Local Similarity 100.0%; Pred. No. 2.3e-91;					
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	GATGACGGCTCAACCATCGCGCCCAACACGGACTATCGCAACACCACTGCTACCGACT	60		
QY	61	ACATCTGCGCTTAATTTACCCCAAGTTTCATGCTTTGTCATGCTGGCGAGCTTGA	120		
DB	61	AAATCTGCGCTTAATTTACCCCAAGTTTCATGCTTTGTCATGCTGGCGAGCTTGA	120		
QY	121	CATGTGGTGGTTTCCCATAGCGCTTATGTTTGTTCCTTATTATTATGTCGCTTATTG	180		
DB	121	CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCGCTTATTG	180		
QY	181	TTGCTTAAAGCGCAGACGGCCAGACCCCCCATCTATAGCGCTTATGTCGCTCAACCC	240		
DB	181	TTGCTTAAAGCGCAGACGGCCAGACCCCCCATCTATAGCGCTTATGTCGCTCAACCC	240		
QY	241	ACCAATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA	300		

Db 241 ACACATGAAATAATTCATAGATTGGACGCTCGAAACCATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
RESULT 2
US-09-814-292-3
; Sequence 3, Application US/09814292
; Patent No. US20020120117A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Zhang, Hong
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 348022001500
; CURRENT APPLICATION NUMBER: US/09/814,292
; CURRENT FILING DATE: 2001-10-12
; PRIOR FILING DATE: 60/191,861
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP
US-09-814-292-3

Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGACGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60
Db 1 GATGACGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120
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Qy 181 TTGCCTAAAGCGCAGACGCGCCACACCCCATCTATAGGCTTATCATTTGCTCAACCC 240
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Qy 241 ACACATGAAATAATTCATAGATTGGACGCTCGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACATGAAATAATTCATAGATTGGACGCTCGAAACCATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 3
US-09-875-228-4
; Sequence 4, Application US/09875228
; Patent No. US20020136707A1
; GENERAL INFORMATION:
; APPLICANT: Yu, D.
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE

; TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
; FILE REFERENCE: 348022000900
; CURRENT APPLICATION NUMBER: US/09/875,228
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/127,834
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 60/076,545
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/054,523
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Adenovirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(307)
US-09-875-228-4
Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGACGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60
Db 1 GATGACGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60
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Qy 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGCTTATTATTATGCGCTTATTG 180
Db 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGCTTATTATTATGCGCTTATTG 180
Qy 181 TTGCCTAAAGCGCAGACGCGCCACACCCCATCTATAGGCTTATCATTTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCACACCCCATCTATAGGCTTATCATTTGCTCAACCC 240
Qy 241 ACACATGAAATAATTCATAGATTGGACGCTCGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACATGAAATAATTCATAGATTGGACGCTCGAAACCATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
RESULT 4
US-09-898-883-22
; Sequence 22, Application US/09898883
; Patent No. US20020164799A1
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/898,883
; APPLICATION NUMBER: US/09/898,883
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SPO
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..304
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-898-883-22

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGCTATCGCAACACCACTGCTACCGGACT 60
DB 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGCTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTGTGCAATGACTGGCGGAGCTTGA 120
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTGTGCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTGCTTATTTATGCTTATTTG 180
DB 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTGCTTATTTATGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCAATCTATAGGCTTATCATTTGCTCAACCC 240
DB 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCAATCTATAGGCTTATCATTTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
DB 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 6
US-09-151-376-61
; Sequence 61, Application US/09151376
; Publication No. US20030044383A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-151-376-61

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGCTATCGCAACACCACTGCTACCGGACT 60
DB 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGCTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTGTGCAATGACTGGCGGAGCTTGA 120
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTGTGCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTGCTTATTTATGCTTATTTG 180
DB 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTGCTTATTTATGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCAATCTATAGGCTTATCATTTGCTCAACCC 240
DB 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCAATCTATAGGCTTATCATTTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
DB 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 5
US-09-151-376-10
; Sequence 10, Application US/09151376
; Publication No. US20030044383A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/09/151,376
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 08/669,753
; EARLIER FILING DATE: 1996-06-26
; EARLIER APPLICATION NUMBER: 08/495,034
; EARLIER FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
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Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Qy 121 CATGTGCTGCTTTCCATAGCGCTTATGTTTGTGCTTATTTATTTATGTCCTTATTTG 180
Db 121 CATGTGCTGCTTTCCATAGCGCTTATGTTTGTGCTTATTTATTTATGTCCTTATTTG 180
Qy 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCGCTATCATTTGTGCTCAACCC 240
Db 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCGCTATCATTTGTGCTCAACCC 240
Qy 241 ACACAATGAAAAAATTCATAGATTGGAATGCGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGAATGCGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
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RESULT 7

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US-09-814-357-17
; Sequence 17, Application US/09814357
; Publication No. US20030068307A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Chen, Yu
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION
; FILE REFERENCE: 348022001600
; CURRENT APPLICATION NUMBER: US/09/814,357
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/192,015
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP
US-09-814-357-17
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Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCATCGCGCCACACGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCACACGGACTATCGCAACACCACTGCTACCGGACT 60

Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120

Qy 121 CATGTGCTGCTTTCCATAGCGCTTATGTTTGTGCTTATTTATTTATGTCCTTATTTG 180
Db 121 CATGTGCTGCTTTCCATAGCGCTTATGTTTGTGCTTATTTATTTATGTCCTTATTTG 180

Qy 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCGCTATCATTTGTGCTCAACCC 240
Db 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCGCTATCATTTGTGCTCAACCC 240

Qy 241 ACACAATGAAAAAATTCATAGATTGGAATGCGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGAATGCGTCTGAAACCAATGTTCTCTTTTACAGTA 300

Qy 301 TGATTAA 307
Db 301 TGATTAA 307
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RESULT 8

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US-09-814-351-17
; Sequence 17, Application US/09814351
; Publication No. US20030148520A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP
US-09-814-351-17
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Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCATCGCGCCACACGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCACACGGACTATCGCAACACCACTGCTACCGGACT 60

Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120

Qy 121 CATGTGCTGCTTTCCATAGCGCTTATGTTTGTGCTTATTTATTTATGTCCTTATTTG 180
Db 121 CATGTGCTGCTTTCCATAGCGCTTATGTTTGTGCTTATTTATTTATGTCCTTATTTG 180

Qy 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCGCTATCATTTGTGCTCAACCC 240
Db 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCGCTATCATTTGTGCTCAACCC 240

Qy 241 ACACAATGAAAAAATTCATAGATTGGAATGCGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGAATGCGTCTGAAACCAATGTTCTCTTTTACAGTA 300

Qy 301 TGATTAA 307
Db 301 TGATTAA 307
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RESULT 9

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US-10-045-116-19
; Sequence 19, Application US/10045116
; Publication No. US20030026792A1
; GENERAL INFORMATION:
; APPLICANT: Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
```

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;
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,116
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..304
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-045-116-19

Query Match 100.0%; Score 307; DB 5; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACGAGCTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACGAGCTATCGCAACACCACTGCTACCGGACT 60

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120

QY 121 CATGTGTGGTGTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCGCTTATTG 180
Db 121 CATGTGTGGTGTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCGCTTATTG 180

QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTCTCAACCC 240

QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 10
US-10-222-479-21
; Sequence 21, Application US/10222479
; Publication No. US20030091538A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS
```

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;
; OF USE
; THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/222,479
; FILING DATE: 16-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/614,495
; FILING DATE: 11-Jul-2000
; APPLICATION NUMBER: 09/033,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2..304
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-222-479-21

Query Match 100.0%; Score 307; DB 5; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACGAGCTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACGAGCTATCGCAACACCACTGCTACCGGACT 60

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120

QY 121 CATGTGTGGTGTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCGCTTATTG 180
Db 121 CATGTGTGGTGTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCGCTTATTG 180

QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTCTCAACCC 240

QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307
Db 301 TGATTAA 307
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RESULT 11
US-10-139-089-10
; Sequence 10, Application US/10139089
; Publication No. US20030152553A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/10/139,089
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; PRIOR APPLICATION NUMBER: 09/509,591
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/033,428
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/033,333
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 60/039,763
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,333
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,762
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)...(304)
US-10-139-089-10

Query Match 100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGACCGGCTCAACCAATCGCGCCCAACCGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCAATCGCGCCCAACCGGACTATCGCAACACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGGGAGCTTGA 120
Qy 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTTATTTATGTTGGCTTATTG 180
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTTATTTATGTTGGCTTATTG 180
Qy 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCAATGCTCAACCC 240
Db 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCAATGCTCAACCC 240
Qy 241 ACACAAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACAAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 12

US-10-139-089-61
; Sequence 61, Application US/10139089
; Publication No. US20030152553A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
; FILE REFERENCE: 348022000221
; CURRENT APPLICATION NUMBER: US/10/139,089
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; PRIOR APPLICATION NUMBER: 09/509,591
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/033,428
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,597
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,555
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,763
; PRIOR FILING DATE: 1997-03-03
; PRIOR APPLICATION NUMBER: 09/033,333
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/039,762
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-139-089-61

Query Match 100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGACCGGCTCAACCAATCGCGCCCAACCGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCAATCGCGCCCAACCGGACTATCGCAACACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGGGAGCTTGA 120
Qy 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTTATTTATGTTGGCTTATTG 180
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTTATTTATGTTGGCTTATTG 180
Qy 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCAATGCTCAACCC 240
Db 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCAATGCTCAACCC 240
Qy 241 ACACAAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACAAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 13
US-10-691-045-17
; Sequence 17, Application US/10691045
; Publication No. US20040146489A1

```

; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/10/691,045
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: US/09/814,351
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP
US-10-691-045-17

Query Match 100.0%; Score 307; DB 7; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60
DB 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60
QY 61 AACATCTGCGCTTAAATTTACCCCAAGTTTCATGCTTGTCAATGAGTGGGCGAGCTTGA 120
DB 61 AACATCTGCGCTTAAATTTACCCCAAGTTTCATGCTTGTCAATGAGTGGGCGAGCTTGA 120
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATATATATGTTGGCTTATTTG 180
DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATATATATGTTGGCTTATTTG 180
QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTGCTCAACCC 240
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 15
US-10-822-873-61
; Sequence 61, Application US/10822873
; Publication No. US20040241857A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown
US-10-822-873-61

Query Match 100.0%; Score 307; DB 8; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60
DB 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60
QY 61 AACATCTGCGCTTAAATTTACCCCAAGTTTCATGCTTGTCAATGAGTGGGCGAGCTTGA 120
DB 61 AACATCTGCGCTTAAATTTACCCCAAGTTTCATGCTTGTCAATGAGTGGGCGAGCTTGA 120
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATATATATGTTGGCTTATTTG 180
DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATATATATGTTGGCTTATTTG 180
QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTGCTCAACCC 240
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 14
US-10-822-873-10
; Sequence 10, Application US/10822873
; Publication No. US20040241857A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0

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Qy	121	CATGTGTGGTGTTCATAGCGCTTATGTTTGTGCTTATTATTATGCTTATTTG	180
Db	121		180
Qy	181	TTGCCCTAAAGCGCAGCGCCAGACCCCCCATCTATAGSCCTATCATTTGTGCTCAACCC	240
Db	181		240
Qy	241	ACACATGGAATAATTCATAGATTGGACGGTCTGAAACCATGTTCTTCTTTTACAGTA	300
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Db	301		307

Search completed: January 20, 2006, 21:23:53
Job time : 806 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:14:55 ; Search time 144 Seconds

(without alignments)
3789.663 Million cell updates/sec

Title: US-10-822-873-10

Perfect score: 307

Sequence: 1 gatgcgggctaaccatcg.....ttctttacagatgattaa 307

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:**

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- 2: /cgn2_6/ptodata/1/ina/5_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	307	3	US-09-033-333-21 Sequence 21, Appl
2	307	100.0	307	3	US-09-033-428-22 Sequence 22, Appl
3	307	100.0	307	3	US-09-033-556-9 Sequence 9, Appl
4	307	100.0	307	3	US-09-614-495-21 Sequence 21, Appl
5	307	100.0	307	3	US-09-898-883-22 Sequence 22, Appl
6	307	100.0	307	3	US-09-151-376-10 Sequence 10, Appl
7	307	100.0	307	3	US-09-151-376-61 Sequence 61, Appl
8	307	100.0	307	3	US-09-814-351-17 Sequence 17, Appl
9	307	100.0	307	3	US-09-814-292-3 Sequence 3, Appl
10	307	100.0	307	3	US-09-392-822A-7 Sequence 7, Appl
11	307	100.0	307	3	US-09-814-357-17 Sequence 17, Appl
12	307	100.0	307	3	US-09-875-228-4 Sequence 4, Appl
13	307	100.0	35937	3	US-09-782-378A-3 Sequence 3, Appl
14	303.8	99.0	34427	3	US-09-111-911-5 Sequence 5, Appl
15	196	63.8	32166	3	US-09-111-911-5 Sequence 11, Appl
16	196	63.8	35408	3	US-09-562-930-11 Sequence 11, Appl
17	196	63.8	35408	3	US-09-873-334-3 Sequence 3, Appl
18	196	63.8	35408	3	US-09-563-869A-3 Sequence 3, Appl
19	196	63.8	35871	3	US-08-549-489-3 Sequence 3, Appl
20	196	63.8	35935	2	US-09-956-335-2 Sequence 2, Appl
21	196	63.8	35935	2	US-08-735-609-1 Sequence 1, Appl
22	196	63.8	35935	3	US-08-379-452-43 Sequence 43, Appl
23	196	63.8	35935	3	US-09-315-372-1 Sequence 1, Appl
24	196	63.8	35935	3	US-09-244-752-1 Sequence 1, Appl

25	196	63.8	35935	3	US-09-245-497-1 Sequence 1, Appl
26	196	63.8	35935	3	US-09-409-670-43 Sequence 43, Appl
27	196	63.8	35935	3	US-09-562-919-1 Sequence 1, Appl
28	196	63.8	35935	3	US-09-782-378A-4 Sequence 4, Appl
29	196	63.8	35935	3	US-09-782-378A-5 Sequence 5, Appl
30	196	63.8	35978	3	US-09-956-335-1 Sequence 1, Appl
31	196	63.8	36620	3	US-09-952-060-30 Sequence 30, Appl
32	196	63.8	37474	3	US-09-952-060-25 Sequence 25, Appl
33	196	63.8	38519	3	US-09-952-060-28 Sequence 28, Appl
34	50	16.3	50	3	US-10-131-827-7472 Sequence 7472, Ap
35	35	11.4	289	3	US-09-007-005-17 Sequence 17, Appl
36	35	11.4	289	3	US-09-244-796-17 Sequence 17565, A
37	33.8	11.0	116955	3	US-09-949-016-17565 Sequence 12504, A
38	32.6	10.6	27684	3	US-09-949-016-17504 Sequence 71369, A
39	31.8	10.4	601	3	US-09-949-016-17504 Sequence 113176, A
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41	31.8	10.4	1494	2	US-09-540-236-216 Sequence 126, App
42	31.8	10.4	2882	2	US-08-724-394A-12 Sequence 12, Appl
43	31.8	10.4	96629	3	US-09-596-002-37 Sequence 17, Appl
44	31.8	10.4	152132	3	US-09-949-016-13845 Sequence 13845, A
45	31.8	10.4	152145	3	US-09-949-016-12371 Sequence 12371, A

ALIGNMENTS

RESULT 1
US-09-033-333-21
; Sequence 21, Application US/09033333
; Patent No. 6197293
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Schuur, Eric
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,333
; FILING DATE: 02-MAR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence

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; LOCATION: 2...304
; OTHER INFORMATION:
US-09-033-333-21

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GATGACGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
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QY 241 ACACATGAAAAAATTCATAGATTGAGCGGTCTGAAACCACTGTTCTCTTTTACAGTA 300
DB 241 ACACATGAAAAAATTCATAGATTGAGCGGTCTGAAACCACTGTTCTCTTTTACAGTA 300
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RESULT 2
US-09-033-428-22
; Sequence 22, Application US/09033428
; Patent No. 6254862
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2...304
US-09-033-428-22

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 ACACATGAAAAAATTCATAGATTGAGCGGTCTGAAACCACTGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 3
US-09-033-556-9
; Sequence 9, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; TITLE OF INVENTION: OF USING SAME
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
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; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...304
; OTHER INFORMATION:
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; US-09-033-556-9
;
; Query Match 100.0%; Score 307; DB 3; Length 307;
; Best Local Similarity 100.0%; Pred. No. 1.6e-97;
; Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGGAATATCGCAACCACTGCTACCGGACT 60
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; QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
; DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
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; QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATTTATGTTGGCTTATTG 180
; DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATTTATGTTGGCTTATTG 180
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; QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGCGCTTATGTTGCTTATTTATTTG 240
; DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGCGCTTATGTTGCTTATTTATTTG 240
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; QY 241 ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCACTGTTCTCTTTTACAGTA 300
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; QY 301 TGATTAA 307
; DB 301 TGATTAA 307
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; RESULT 4
; US-09-614-495-21
; Sequence 21, Application US/09614495
; Patent No. 6436394
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
;
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; THEREOF
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/614,495
; FILING DATE: 11-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/033,333
; FILING DATE: <Unknown>
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; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
;
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...304
; OTHER INFORMATION:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
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; US-09-614-495-21
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; Query Match 100.0%; Score 307; DB 3; Length 307;
; Best Local Similarity 100.0%; Pred. No. 1.6e-97;
; Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGGAATATCGCAACCACTGCTACCGGACT 60
; DB 1 GATGACCGGCTCAACCATCGCGCCCAACACGGAATATCGCAACCACTGCTACCGGACT 60
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; QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
; DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
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; QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATTTATGTTGGCTTATTG 180
; DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATTTATGTTGGCTTATTG 180
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; QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGCGCTTATGTTGCTTATTTATTTG 240
; DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGCGCTTATGTTGCTTATTTATTTG 240
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; QY 241 ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCACTGTTCTCTTTTACAGTA 300
; DB 241 ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCACTGTTCTCTTTTACAGTA 300
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; QY 301 TGATTAA 307
; DB 301 TGATTAA 307
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; RESULT 5
; US-09-898-883-22
; Sequence 22, Application US/09898883
; Patent No. 6585968
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; Lamparski, Henry
; Schuur, Eric
; Henderson, Daniel
;
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
;
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,883
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/033,428
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POLIZZIO, CATHERINE M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 34802-30004.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 2..304
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-898-883-22

Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTGCTTATTTATGCTTATTG 120
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTGCTTATTTATGCTTATTG 120
QY 121 CATGTGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGCTTATTG 180
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QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTTTTACAGTA 300
DB 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 6
US-09-151-376-10
Sequence 10, Application US/09151376
Patent No. 6676935
GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
APPLICANT: Schuur, E.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REFERENCE: 34802200221
CURRENT APPLICATION NUMBER: US/09/151,376
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 08/669,753
EARLIER FILING DATE: 1996-06-26
EARLIER APPLICATION NUMBER: 08/495,034
EARLIER FILING DATE: 1995-06-27
NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 307
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(304)
US-09-151-376-10

Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
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DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTCAATGACTGGGCGAGCTTGA 120
QY 121 CATGTGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGCTTATTG 180
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DB 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 7
US-09-151-376-61
Sequence 61, Application US/09151376
Patent No. 6676935
GENERAL INFORMATION:
APPLICANT: Henderson, D.R.
APPLICANT: Schuur, E.R.
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
FILE REFERENCE: 34802200221
CURRENT APPLICATION NUMBER: US/09/151,376
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 08/669,753
EARLIER FILING DATE: 1996-06-26
EARLIER APPLICATION NUMBER: 08/495,034
EARLIER FILING DATE: 1995-06-27
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61
LENGTH: 307
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-151-376-61

Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
DB 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTCAATGACTGGGCGAGCTTGA 120

Db 61 AACATCGCCCTAAATTTACCCAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGTTGCTTATTTG 180
Db 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGTTGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGACGGCGCCAGACCCCATCTATAGCCCTCATCTGTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGGCGCCAGACCCCATCTATAGCCCTCATCTGTGCTCAACCC 240
QY 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 8

US-09-814-351-17
; Sequence 17, Application US/09814351
; Patent No. 6692736
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP

US-09-814-351-17

Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGTTGCTTATTTG 180
Db 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGTTGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGACGGCGCCAGACCCCATCTATAGCCCTCATCTGTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGGCGCCAGACCCCATCTATAGCCCTCATCTGTGCTCAACCC 240
QY 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 9

US-09-814-292-3
; Sequence 3, Application US/09814292
; Patent No. 6852528
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Zhang, Hong
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 348022001500
; CURRENT APPLICATION NUMBER: US/09/814,292
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/191,861
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP

US-09-814-292-3

Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGTTGCTTATTTG 180
Db 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGTTGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGACGGCGCCAGACCCCATCTATAGCCCTCATCTGTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGGCGCCAGACCCCATCTATAGCCCTCATCTGTGCTCAACCC 240
QY 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 10

US-09-392-822A-7
; Sequence 7, Application US/09392822A
; Patent No. 6900049
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: Adenovirus Vectors Containing Cell
; TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
; FILE REFERENCE: CELL-014; 122.1
; CURRENT APPLICATION NUMBER: US/09/392,822A
; CURRENT FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/099,791
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/392,822
; PRIOR FILING DATE: 1999-09-09

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Adenovirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(304)
US-09-392-822A-7

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCAATTCAGGACTATCGCAACGAGTATCGCAACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCAATTCAGGACTATCGCAACGAGTATCGCAACCACTGCTACCGGACT 60

Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGGGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGGGA 120

Qy 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATTTATGTTGCTTATTTG 180
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATTTATGTTGCTTATTTG 180

Qy 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240

Qy 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300

Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 12
US-09-875-228-4
; Sequence 4, Application US/09875228
; Patent No. 6916918
; GENERAL INFORMATION:
; APPLICANT: Yu, D.
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE
; TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF
; FILE REFERENCE: 348022000900
; CURRENT APPLICATION NUMBER: US/09/875, 228
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/127,834
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: 60/076,545
; PRIOR FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: 60/054,523
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Adenovirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(307)
US-09-875-228-4

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCAATTCAGGACTATCGCAACGAGTATCGCAACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCAATTCAGGACTATCGCAACGAGTATCGCAACCACTGCTACCGGACT 60

Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGGGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGGGA 120

Qy 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATTTATGTTGCTTATTTG 180
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATTTATGTTGCTTATTTG 180

Qy 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240

Qy 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300

Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 11
US-09-814-357-17
; Sequence 17, Application US/09814357
; Patent No. 6911200
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Chen, Yu
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION
; FILE REFERENCE: 348022001600
; CURRENT APPLICATION NUMBER: US/09/814,357
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP
US-09-814-357-17

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCAATTCAGGACTATCGCAACGAGTATCGCAACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCAATTCAGGACTATCGCAACGAGTATCGCAACCACTGCTACCGGACT 60
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Db      241  ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Qy      301  TGATTAA 307
Db      301  TGATTAA 307

RESULT 13
US-09-111-911-5/c
; Sequence 3, Application US/09782378A-3
; Patent No. 6916635
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandelon, Ziv
; APPLICANT: Gnatenko, Dmitri
; FILE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; CURRENT FILING DATE: 2001-02-12
; PRIOR FILING DATE: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 35937
; TYPE: DNA
; ORGANISM: Human adeno-associated virus 2
US-09-782-378A-3

Query Match      100.0%; Score 307; DB 3; Length 35937;
Best Local Similarity 100.0%; Pred. No. 1.9e-96;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GATGACCGGCTCAACCATCGCGCCCAACGGACTATCGCAACACCACTGCTACCGGACT 60
Db      29467 GATGACCGGCTCAACCATCGCGCCCAACGGACTATCGCAACACCACTGCTACCGGACT 29526

Qy      61  AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTTGGA 120
Db      29527 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTTGGA 29586

Qy      121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATTTATTTATGTTGGCTTTATTG 180
Db      29587 CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATTTATTTATGTTGGCTTTATTG 29646

Qy      181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db      29647 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 29706

Qy      241 ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db      29707 ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 29766

Qy      301  TGATTAA 307
Db      29767 TGATTAA 29773

RESULT 14
US-09-111-911-5/c
; Sequence 5, Application US/09111911
; Patent No. 6881402
; GENERAL INFORMATION:
; APPLICANT: Wold, William S.M.
; FILE OF INVENTION: Inhibiting Apoptosis With Adenovirus RID Protein
; FILE REFERENCE: 16153-5587
; CURRENT APPLICATION NUMBER: US/09/111,911
; CURRENT FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5

Db      241  ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Qy      301  TGATTAA 307
Db      301  TGATTAA 307

; LENGTH: 34427
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: Combining E.coli and Adenovirus Sequences
US-09-111-911-5

Query Match      99.0%; Score 303.8; DB 3; Length 34427;
Best Local Similarity 99.3%; Pred. No. 2.5e-95;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GATGACCGGCTCAACCATCGCGCCCAACGGACTATCGCAACACCACTGCTACCGGACT 60
Db      1996 GTTGACCGGCTCAACCATCGCGCCCAACGGACTATCGCAACACCACTGCTACCGGACT 1937

Qy      61  AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTTGGA 120
Db      1936 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTTGGA 1877

Qy      121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATTTATTTATGTTGGCTTTATTG 180
Db      1876 CTTGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATTTATTTATGTTGGCTTTATTG 1817

Qy      181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db      1816 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 1757

Qy      241 ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db      1756 ACACATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 1697

Qy      301  TGATTAA 307
Db      1696 TGATTAA 1690

RESULT 15
US-09-562-930-11
; Sequence 11, Application US/09562930
; Patent No. 6835812
; GENERAL INFORMATION:
; APPLICANT: Genotherapeutics Inc.
; APPLICANT: Steiner, Mitchell
; APPLICANT: Wang, Chiang
; APPLICANT: Rinaldy, Augustinus
; APPLICANT: Menon, Rema
; TITLE OF INVENTION: Isolated nucleic acids of the p-hyde family, p-hyde proteins, and
; TITLE OF INVENTION: of inducing susceptibility to induction of cell death in cancer
; FILE REFERENCE: P-2762-US2
; CURRENT APPLICATION NUMBER: US/09/562,930
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 09/302,457
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: US 09/499,817
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 32166
; TYPE: DNA
; ORGANISM: Rat
US-09-562-930-11

Query Match      63.8%; Score 196; DB 3; Length 32166;
Best Local Similarity 86.4%; Pred. No. 1.7e-57;
Matches 228; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

Qy      45  CCACTGCTACCGGACTTAACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATG 104
Db      26180 CCGCCGCTACCGGACTTACATCTACCACAAATACACCCCAAGTTTCTGCTTTGTCAATA 26239

Qy      105  ACTGGGCGAGCTTGGACATGTGGTGGTTTTCATAGCGCTTATGTTGTTGCTTATTA 164
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Db      26240  ACTGGGATAACTTGGGCATGTGGTGGTTCTCCATAGCGCTTATGTTGTATGCTTATTA 26299
Qy      165  TTATGTGGCTTATTTGTTCCTAAAGCGCAGAGCGCCAGACCCGCCCATCTATAGGCCTA 224
Db      26300  TTATGTGGCTCATCTGCTGCTAAAGCGCAAAGCGCCGACCCCATCTATAGTCCCA 26359
Qy      225  TCATTGTGCTCAACCCACACAATGMAAAATTCATAGATTGGACGGTCTGAAAC-CATGT 283
Db      26360  TCATTGTGCTACACCCCAACANTGATGGAAATCCATAGATTGGACGGACTGAAACACATGT 26419
Qy      284  TCTCTTCTTTTACAGTATGATTAA 307
Db      26420  TCTTTCTCTTACAGTATGATTAA 26443

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Search completed: January 20, 2006, 21:10:15
 Job time : 147 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 17:03:15 ; Search time 472 Seconds
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4334.874 Million cell updates/sec

Title: US-10-822-873-10
Perfect score: 307
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Scoring table: IDENTITY_NUC

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: Geneseqn1980s.*
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5: Geneseqn2001bs.*
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7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
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13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	307	100.0	307	2	AAV47675
2	307	100.0	307	2	AAV52966
3	307	100.0	307	2	AAV57354
4	307	100.0	307	2	AAV24756
5	307	100.0	307	3	AAZ99937
6	307	100.0	307	3	AAZ99937
7	307	100.0	307	5	AAH43535
8	307	100.0	307	6	ABK99587
9	307	100.0	307	8	ACD07312
10	307	100.0	307	12	ADI36397
11	307	100.0	307	12	ADI36417
12	307	100.0	307	14	ADV21029
13	307	100.0	307	14	ADW47774
14	307	100.0	307	14	ADW47774
15	307	100.0	917	14	ADW28317
16	307	100.0	34616	6	ABK49009
17	307	100.0	35209	14	ADW28315
18	307	100.0	35937	6	ABS69881
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21	305.4	99.5	307	2	AAV53632	AAV53632 Adenoviru
c 22	303.8	99.0	34427	2	AAV53632	AAV53632 Adenoviru
c 23	303.8	99.0	34427	9	ADA09839	Ada09839 Adenoviru
24	303	98.7	303	14	ADM28319	Adm28319 Nucleotid
25	302.2	98.4	35759	10	ADF60698	Adf60698 Ad6 genom
26	302.2	98.4	35759	13	ADS00148	AdS00148 Human ade
27	196	63.8	32165	3	AAA09092	Aaa09092 AdMTV-be
28	196	63.8	32165	3	AAA14723	Aaa14723 Nucleotid
29	196	63.8	32166	3	AAA09090	Aaa09090 AdPSA-bet
30	196	63.8	32166	4	AAC89170	Aac89170 ADRSVpHYD
31	196	63.8	32166	14	ADM11287	Adm11287 Adenovira
32	196	63.8	32167	3	AAA14803	Aaa14803 Nucleotid
33	196	63.8	32167	3	AAZ93332	Aaz93332 Partial s
34	196	63.8	32886	3	AAA09086	Aaa09086 ADRSV-bet
35	196	63.8	33592	4	AAC85018	Aac85018 Adenoviru
36	196	63.8	33699	4	AAC85020	Aac85020 Adenoviru
37	196	63.8	33988	4	AAC85023	Aac85023 Adenoviru
38	196	63.8	34302	3	AAZ94163	Aaz94163 Adenoviru
39	196	63.8	34341	4	AAC85019	Aac85019 Adenoviru
40	196	63.8	34448	4	AAC85021	Aac85021 Adenoviru
41	196	63.8	34737	4	AAC85024	Aac85024 Adenoviru
42	196	63.8	35408	2	AAV59272	AAV59272 Recombina
43	196	63.8	35620	14	ADY80723	Ady80723 DNA seque
44	196	63.8	35700	14	ADY93032	Ady93032 Human ade
45	196	63.8	35712	14	ADZ45246	Adz45246 Human ade

ALIGNMENTS

RESULT 1
AAV47675
ID AAV47675 standard; DNA; 307 BP.

XX AAV47675;

XX 27-AUG-2003 (revised)
DT 07-DEC-1998 (first entry)

XX Adenovirus death protein gene.

XX Adenovirus death protein; ADP; vector; hepatoma; cancer;
KW alpha-fetoprotein transcription regulatory element; AFP-TRE;
KW hepatocellular carcinoma; hepatoma; gene therapy; human; ds.
XX Mastadenovirus.

XX Key Location/Qualifiers
FH CDS 2..307
FT FT /*tag= a

XX WO9839465-A2.

XX 11-SEP-1998.

XX 03-MAR-1998; 98WO-US004084.

XX 03-MAR-1997; 97US-0039597P.

XX 02-MAR-1998; 98US-00033428.

XX (CALY-) CALYDON INC.

XX Little AS, Lamparski HG, Henderson DR, Schuur ER;

XX WPI; 1998-495861/42.

XX P-PSDB; AAW61197.

XX New adenovirus vector, for treating cancers - comprising an adenovirus
PT gene under the transcriptional control of an alpha fetoprotein
PT transcription regulatory element.

XX Claim 31; Page 74; 102pp; English.

XX This nucleotide sequence codes for adenovirus death protein (ADP, see
CC AAV61197) of adenovirus type 2. The ADP coding sequence (with or without
CC the Y leader) can be introduced into an adenoviral genome, e.g. in the E3
CC or E4 region. Inclusion of such a coding sequence in an adenoviral vector
CC significantly enhances the extent of cytotoxicity, cell killing and virus
CC production. The invention provides replication-competent adenovirus
CC vectors which preferentially replicate in cells that express alpha-
CC fetoprotein (AFP), particularly hepatoma cells. The vectors comprise at
CC least one adenovirus gene, preferably a gene that contributes to
CC cytotoxicity, under the transcriptional control of an AFP transcription
CC regulatory element (see AAV47654-55). The vectors are useful for
CC conferring selective cytotoxicity to AFP-expressing cells, especially
CC cancer cells. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGACTATCGCAACCACTGCTACCGGACT 60
DB |||||||
1 GATGACCGGCTCAACCATCGCGCCACACGAGACTATCGCAACCACTGCTACCGGACT 60

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120
DB |||||||
61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120

QY 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTGTTGGCTTATTATTATGTCCTATTG 180
DB |||||||
121 CATGTGGTGGTTTTCCATAGCGCTTATGTTGTTGGCTTATTATTATGTCCTATTG 180

QY 181 TTGCTTAAAGCGAGAGCGCGCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240
DB |||||||
181 TTGCTTAAAGCGAGAGCGCGCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240

QY 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
DB |||||||
241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307
DB |||||||
301 TGATTAA 307

RESULT 2
AAV52966
ID AAV52966 standard; DNA; 307 BP.
XX
AC AAV52966;
XX
XX 21-DEC-1998 (first entry)
XX
XX Adenovirus death protein gene coding region.
XX
XX Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE;
XX human; promoter; enhancer; vector; cancer; gene therapy; PCR; primer;
XX adenovirus death protein; ADP; ds.
XX
XX Mastadenovirus.
XX
XX Key Location/Qualifiers
XX CDS 2..304
XX /*tag= a
XX
XX WO9839467-A2.
XX
XX 11-SEP-1998.
XX
XX 03-MAR-1998; 98WO-US004133.
XX
XX 03-MAR-1997; 97US-0039763P.
XX
PR

PR 02-MAR-1998; 98US-00033555.
XX (CALY-) CALYDON INC.
XX Lamparski HG, Henerson DR, Schuur ER;
XX WPI; 1998-495862/42.
DR P-PSDB; AAV78902.
XX
XX New adenovirus vectors, particularly for cancer therapy - comprising
PT adenovirus gene under transcriptional control of carcinoembryonic antigen
PT transcriptional regulatory element.
XX
XX Disclosure; Page 67-68; 95pp; English.
XX
CC This is the coding region of the adenovirus death protein (ADP, see
CC AAV78902). It can be obtained by PCR amplification (see also AAV52945-
CC 46). Claimed replication-competent adenovirus (Ad) vectors comprise an Ad
CC gene under transcriptional control of a CEA-TRE. The vectors can be used
CC to detect and monitor samples for the presence of cells that allow a CEA-
CC TRG to function, and to selectively kill such cells, especially malignant
CC cells. Vectors containing an ADP gene may be more potent than vectors
CC lacking the gene, making possible more effective treatment and/or lower
CC dosage requirement
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGACTATCGCAACCACTGCTACCGGACT 60
DB |||||||
1 GATGACCGGCTCAACCATCGCGCCACACGAGACTATCGCAACCACTGCTACCGGACT 60

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120
DB |||||||
61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120

QY 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTGTTGGCTTATTATTATGTCCTATTG 180
DB |||||||
121 CATGTGGTGGTTTTCCATAGCGCTTATGTTGTTGGCTTATTATTATGTCCTATTG 180

QY 181 TTGCTTAAAGCGAGAGCGCGCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240
DB |||||||
181 TTGCTTAAAGCGAGAGCGCGCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240

QY 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
DB |||||||
241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307
DB |||||||
301 TGATTAA 307

RESULT 3
AAV57354
ID AAV57354 standard; DNA; 307 BP.
XX
AC AAV57354;
XX
XX 21-DEC-1998 (first entry)
XX
XX Adenovirus death protein gene coding region.
XX
XX Probasin transcriptional response element; PB-TRE; rat;
XX androgen receptor; adenovirus; vector; prostate cancer; gene therapy;
XX adenovirus death protein; ADP; ss.
XX
XX Mastadenovirus.
XX
XX Key Location/Qualifiers
XX FH

[illegible]

RESULT 4
AAX24756
ID AAX24756 standard; DNA; 307 BP.

```
QY 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 5
AAZ99937
ID AAZ99937 standard; DNA; 307 bp.
XX
AC AAZ99937;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA encoding an adenoviral death protein.
XX
KW adenoviral vector; adenovirus gene; transcriptional control;
KW transcriptional regulatory element; TRE; adenoviral propagation;
KW death protein; tumour; ss.
XX
OS Mastadenovirus.
XX
XX Key Location/Qualifiers
FH CDS 2..307
FT /*tag= a
FT /product= "death protein"
XX
XX WO200015820-A1.
XX
XX 23-MAR-2000.
XX
XX 10-SEP-1999; 99WO-US020718.
XX
XX 10-SEP-1998; 98US-0099791P.
XX 09-SEP-1999; 99US-00392822.
XX
XX (CALY-) CALYDON INC.
XX
XX Yu DC, Henderson DR;
XX
XX WPI; 2000-271456/23.
XX P-PSDB; AAY84407.
XX
XX Adenovirus vectors comprising cell-status specific response elements
XX useful in gene therapy protocols for the treatment of cancers.
XX
XX Disclosure; Fig 9; 79pp; English.
XX
XX The present sequence encodes an adenoviral death protein, which is used
XX to construct the vectors of the invention. The specification describes
XX adenoviral vectors which comprise an adenovirus gene under
XX transcriptional control of a cell status specific transcriptional
XX regulatory element (TRE). The TRE is preferably one that is essential for
XX adenoviral propagation. The adenovirus vectors may be used for the
XX treatment of a range of tumours such as lung, stomach, breast, colon and
XX rectum, and uterine and cervix cancers
XX
XX Sequence 307 bp; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATCAGCGGCTCAACCATCGGCCCAACACGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATCAGCGGCTCAACCATCGGCCCAACACGGACTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGA 120
120
```

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Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTCCCATAGCGCTTATGTTTGGCTTATTATTATGCGCTTATTG 180
Db 121 CATGTGGTGGTTTCCCATAGCGCTTATGTTTGGCTTATTATTATGCGCTTATTG 180
QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCGCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCGCCATCTATAGCCCTATCATTTGCTCAACCC 240
QY 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 6
AAI70186
ID AAI70186 standard; DNA; 307 bp.
XX
AC AAI70186;
XX
DT 11-SEP-2003 (revised)
DT 07-JAN-2002 (first entry)
XX
DE Adenovirus death protein gene.
XX
DE Adenovirus death protein; uroplakin II; vector;
KW transcriptional regulatory element; TRE; urothelial cell; bladder cancer;
KW human; gene therapy; ss.
XX
XX Human adenovirus type 2.
XX
XX Key Location/Qualifiers
FH CDS 2..307
FT /*tag= a
XX
XX WO200172994-A2.
XX
XX 04-OCT-2001.
XX
XX 21-MAR-2001; 2001WO-US009224.
XX
XX 24-MAR-2000; 2000US-0191861P.
XX
XX (CALY-) CALYDON INC.
XX
XX Yu D, Zhang H, Henderson DR;
XX
XX WPI; 2001-639229/73.
XX P-PSDB; AAM50206.
XX
XX Human urothelial cell specific uroplakin transcriptional regulatory
XX sequences, useful for producing adenoviral vectors which can be used to
XX confer selective cytotoxicity to target cells, especially bladder cancer
XX cells.
XX
XX Example 6; Fig 12; 147pp; English.
XX
XX The present sequence is that of the coding region of the adenovirus death
XX protein. The sequence was obtained by PCR amplification and used in the
XX construction of adenoviral vectors in which ADP expression and used in the
XX control of a urothelial cell-specific transcriptional regulatory element
XX (TRE) derived from the human uroplakin II gene 5' flanking region (see
XX AAI70144). This is an example of adenoviral vectors of the invention.
XX Such vectors comprise a gene, preferably an adenovirus gene, under
XX transcriptional control of a urothelial cell-specific TRE. They display
XX urothelial cell-specific cytotoxicity, and are used for the specific,
XX targeted gene therapy of bladder cancer. (Updated on 11-SEP-2003 to
XX standardise OS field)
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XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match      100.0%; Score 307; DB 4; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACGCGACTATCGCAACCACTGCTACCGGACT 60
DB 1 GATGACCGGCTCAACCATCGCGCCCAACGCGACTATCGCAACCACTGCTACCGGACT 60

QY 61 AACATCTGCGCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
DB 61 AACATCTGCGCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120

QY 121 CATGTGTGTTTTCATAGCGCTTATGTTTGTGCTTATTTATATGTTGGCTTATTTG 180
DB 121 CATGTGTGTTTTCATAGCGCTTATGTTTGTGCTTATTTATATGTTGGCTTATTTG 180

QY 181 TTGCCTAAAGCGCAGACGCGCCCAACGCGCTTATAGCCCTATCATTTGCTCAACCC 240
DB 181 TTGCCTAAAGCGCAGACGCGCCCAACGCGCTTATAGCCCTATCATTTGCTCAACCC 240

QY 241 ACACAATGAAATAATTTCATAGATTGACGCTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
DB 241 ACACAATGAAATAATTTCATAGATTGACGCTCTGAAACCAATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 7
AAH43535
ID AAH43535 standard; cDNA; 307 BP.
AC AAH43535;
XX
XX
DT 11-SEP-2003 (revised)
DT 07-JAN-2002 (first entry)
DE ADP nucleotide sequence.
XX
XX Adenovirus; ADP; replication-competent; adenoviral vector; TRE;
XX transcriptional regulatory element; mutation; deletion; IRES; promoter;
XX internal ribosome entry site; cytotoxic; cancer; bladder; ss.
XX
XX unidentified adenovirus.
XX
XX Key Location/Qualifiers
FH CDS 2..307
FT /*tag= a
FT /product= "ADP"
XX
XX WC200173093-A2.
XX
XX 04-OCT-2001.
XX
XX 21-MAR-2001; 2001WO-US009036.
XX
XX 24-MAR-2000; 2000US-0192156P.
XX
XX (CALY-) CALYDON INC.
XX
XX Yu D, Li Y, Henderson DR;
XX
XX WPI; 2001-639234/73.
DR P-PSDB; AAB47591.
XX
XX Replication-competent adenoviral vector, useful e.g. for killing cancer
XX cells, contains two genes linked by internal ribosome entry site and
XX controlled by target-specific regulator.
XX

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PS Disclosure; Fig 9; 148pp; English.
XX
CC This sequence encodes adenoviral ADP. This coding sequence may be used in
CC the replication-competent adenoviral vector (A) of the invention which
CC contains two genes (G1, G2) that are co-transcribed as a single mRNA and
CC under control of a heterologous, target cell-specific transcriptional
CC regulatory element (TRE). G2 has a mutation in, or deletion of, its
CC endogenous promoter and is controlled from an internal ribosome entry
CC site (IRES). The ADP coding sequence may be used as G1 or G2. (A) has
CC greater specificity for a target cell than a similar vector in which TRE
CC is operably linked to a gene and which lacks an IRES. (A) are used to
CC modify the genotype of target cells, optionally in vitro with subsequent
CC return of altered cells to the host and where G2 is a cytotoxic gene, to
CC confer selective cytotoxicity to target cells, especially for killing
CC cancer cells. ADP displays a cytotoxic, particularly cell lysis,
CC function. Also (A) are used for diagnosis and monitoring, e.g. detection
CC of bladder cancer cells. The target cell-specific TRE ensures that (A)
CC has better targeting specificity, with minimal replication in non-target
CC cells, so a runaway infection is prevented but production of adenoviral
CC proteins in target cells activates and/or stimulates the immune response
CC against target cells producing such proteins. The use of an IRES (rather
CC than two identical control elements) eliminates the risk of homologous
CC recombination and may provide enough extra space for an additional
CC (therapeutic) gene. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match      100.0%; Score 307; DB 5; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACGCGACTATCGCAACCACTGCTACCGGACT 60
DB 1 GATGACCGGCTCAACCATCGCGCCCAACGCGACTATCGCAACCACTGCTACCGGACT 60

QY 61 AACATCTGCGCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
DB 61 AACATCTGCGCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120

QY 121 CATGTGTGTTTTCATAGCGCTTATGTTTGTGCTTATTTATATGTTGGCTTATTTG 180
DB 121 CATGTGTGTTTTCATAGCGCTTATGTTTGTGCTTATTTATATGTTGGCTTATTTG 180

QY 181 TTGCCTAAAGCGCAGACGCGCCCAACGCGCTTATAGCCCTATCATTTGCTCAACCC 240
DB 181 TTGCCTAAAGCGCAGACGCGCCCAACGCGCTTATAGCCCTATCATTTGCTCAACCC 240

QY 241 ACACAATGAAATAATTTCATAGATTGACGCTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
DB 241 ACACAATGAAATAATTTCATAGATTGACGCTCTGAAACCAATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 8
ABK99587
ID ABK99587 standard; DNA; 307 BP.
XX
XX ABK99587;
AC ABK99587;
XX
XX 21-OCT-2002 (first entry)
XX
XX DNA encoding adenovirus death protein (ADP).
XX
XX Adenovirus; transcriptional regulatory element; TRE; prostate; liver;
XX breast cancer; colon cancer; antitumor; gene; ds; probasin; PB; human;
XX rat; carcinoembryonic antigen; prostate-specific antigen; ADP;
XX adenovirus death protein; glandular kallikrein.
XX
XX Unidentified.
XX

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PN US2002068049-A1.
XX 06-JUN-2002.
XX 06-DEC-2000; 2000US-00732169.
XX 10-SEP-1998; 98US-00151376.
XX (HEND/) HENDERSON D R.
XX (SCHU/) SCHUUR E R.
XX Henderson DR, Schuur ER;
XX WPI: 2002-582468/62.
XX P-PSDB; ABG69353.
XX Novel adenovirus vector comprises adenovirus gene under transcriptional
PT control of cell-type specific transcriptional response element for
PT conferring selective toxicity on target cell and for suppressing tumor
PT growth.
XX Disclosure; Fig 19; 83pp; English.
XX The invention relates to an adenovirus vector (AV) comprising an AV gene
CC under transcriptional control of a cell type-specific transcriptional
CC regulatory element (TRE) and optionally a first AV gene under control of
CC a first cell type-specific TRE and a second gene under control of a
CC second cell type-specific TRE, where the first and second cell type-
CC specific TREs are substantially identical. When the vector is introduced
CC into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon
CC cancer cell) it allows the cell type-specific TRE to function, resulting
CC in cytotoxicity. The vector is useful for suppressing tumour growth of a
CC target cell. This sequence represents a polynucleotide used in the scope
CC of the invention
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
Query Match 100.0%; Score 307; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCCCTTTGTCAATGACTGGGCGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCCCTTTGTCAATGACTGGGCGAGCTTGA 120
Qy 121 CATGTGTGGTGTTCATAGGCTTATGTTTGTGCTTATTTATGCTTATTTG 180
Db 121 CATGTGTGGTGTTCATAGGCTTATGTTTGTGCTTATTTATGCTTATTTG 180
Qy 181 TTGCTTAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATGCTTCAACCC 240
Db 181 TTGCTTAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATGCTTCAACCC 240
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
RESULT 9
ACD07312
ID ACD07312 standard; DNA; 307 BP.
XX
AC ACD07312;
XX
DT 27-OCT-2003 (revised)
DT 07-AUG-2003 (first entry)
XX DNA encoding adenovirus death protein (ADP).
XX Adenoviral vector; adenovirus gene; transcriptional control; TRE;
KW cell type-specific; transcriptional response element; PSA; hKLUK;
KW prostate-specific antigen; glandular kallikrein; probastin; PB;
KW carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1;
KW cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic;
KW adenovirus death protein; ADP; gene; ds.
XX unidentified adenovirus.
XX US2003044383-A1.
XX 06-MAR-2003.
XX 10-SEP-1998; 98US-00151376.
XX 27-JUN-1995; 95US-00495034.
XX 20-AUG-1996; 96US-00699753.
XX 03-MAR-1997; 97US-0039597P.
XX 03-MAR-1997; 97US-0039599P.
XX 03-MAR-1997; 97US-0039762P.
XX 03-MAR-1997; 97US-0039763P.
XX 02-MAR-1998; 98US-00033333.
XX 02-MAR-1998; 98US-00033428.
XX 02-MAR-1998; 98US-00033555.
XX (HEND/) HENDERSON D R.
XX (SCHU/) SCHUUR E R.
XX Henderson DR, Schuur ER;
XX WPI: 2003-456547/43.
XX P-PSDB; ABU10308.
XX New adenovirus vector for transfecting target host cells, comprises an
PT adenovirus gene under transcriptional control of a cell type-specific
PT transcriptional response element.
XX Disclosure; Fig 19; 83pp; English.
XX The present invention relates to adenoviral vectors comprising an
CC adenovirus gene under transcriptional control of a cell type-specific
CC transcriptional response element (TRE). Example TREs given in the
CC specification include human prostate-specific antigen (PSA) TRE, human
CC glandular kallikrein (hKLUK) TRE, rat probastin (PB) TRE, human
CC carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3
CC (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for
CC introducing new genetic capability, particularly associated with
CC cytotoxicity for treating neoplasia. For example, the vector may be used
CC in a target cell to suppress tumour growth, or to kill the target cell.
CC The vector is particularly useful in gene therapy. The present sequence
CC encodes adenovirus death protein (ADP). (Updated on 27-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
Query Match 100.0%; Score 307; DB 8; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCCCTTTGTCAATGACTGGGCGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCCCTTTGTCAATGACTGGGCGAGCTTGA 120
Qy 121 CATGTGTGGTGTTCATAGGCTTATGTTTGTGCTTATTTATGCTTATTTG 180
Db 121 CATGTGTGGTGTTCATAGGCTTATGTTTGTGCTTATTTATGCTTATTTG 180

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Db 121 CATGTGGTGTTCATAGCGCTATGTTGTTGGCTTATTATTATGAGGCTTATTG 180
Qy 181 TTGCTTAAAGCGCAGAGCGCCAGACCCCACTATATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCTTAAAGCGCAGAGCGCCAGACCCCACTATATAGCCCTATCATTTGCTCAACCC 240
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCAATGTTCTTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCAATGTTCTTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 10
AD136397
ID AD136397 standard; DNA; 307 BP.
XX
AC AD136397;
XX
DT 22-APR-2004 (first entry)
XX
DE Human mucin (MUC1) transcriptional response element DNA SeqID61.
XX
KW ds; mucin; MUC1; human; prostate; transcriptional response element; TRE;
KW polyethylene glycol; PEG; masking agent; tumour cell growth;
KW proliferation; psoriatic lesion; wound healing; hyperplasia; cancer;
KW cytotatic; antipsoriatic; vulnery; human.
XX
OS Homo sapiens.
XX
PN US2003152553-A1.
XX
PD 14-AUG-2003.
XX
PF 02-MAY-2002; 2002US-00139089.
XX
PR 27-JUN-1995; 95US-00495034.
PR 26-JUN-1996; 96US-00669753.
PR 03-MAR-1997; 97US-0039597P.
PR 03-MAR-1997; 97US-0039762P.
PR 03-MAR-1997; 97US-0039763P.
PR 02-MAR-1998; 98US-00033333.
PR 02-MAR-1998; 98US-00033428.
PR 02-MAR-1998; 98US-00033555.
PR 10-SEP-1998; 98US-00151376.
PR 02-JUN-2000; 2000US-00509591.
XX
PA (LITV/) LITTLE A S.
PA (LAMP/) LAMPARSKI H G.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
XX
PI Little AS, Lamparski HG, Henderson DR, Schuur ER;
XX
XX WPI; 2004-119002/12.
XX
XX Composition comprising replication competent adenovirus having adenovirus
XX PT gene essential for replication under transcriptional control of cell type
XX PT specific transcriptional response element and masking agent.
XX
XX Example 5; SEQ ID NO 61; 115pp; English.
XX
XX This invention relates to a novel composition that contains a replication
XX CC competent adenovirus capable of transfecting target host cells.
XX CC Specifically, it comprises an adenoviral gene essential for replication
XX CC (51A, E1B or E4), which is under the transcriptional control of a
XX CC prostate specific transcriptional response element (TRE) and polyethylene
XX CC glycol (PEG) as the masking agent. The present invention describes this
XX CC composition as useful for suppressing tumour cell growth and for lowering
XX CC the levels of tumour cell markers. It can also be used for introducing
XX CC transient expression that may be involved in treating undesired
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CC proliferations other than tumours, such as psoriatic lesions and wound
CC healing. In addition, it is useful for detecting cells where a cell type-
CC specific TRE is functional in a biological sample and for treating
CC prostate-associated diseases such as hyperplasia and cancer. As such,
CC these compositions exhibit cytostatic, antipsoriatic and vulnery
CC activities. This polynucleotide sequence is the human mucin (MUC1) TRE
CC DNA sequence of the invention. NOTE: This sequence is identical to that
CC given as SeqID 10.
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 12; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCATCGCGCCCAACGCGACTATGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACGCGACTATGCAACACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCAATGCTTTGTCAATGACTGGGCGGACTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCAATGCTTTGTCAATGACTGGGCGGACTTGA 120
Qy 121 CATGTGGTGTTCATAGCGCTATGTTGTTGGCTTATTATTATGAGGCTTATTG 180
Db 121 CATGTGGTGTTCATAGCGCTATGTTGTTGGCTTATTATTATGAGGCTTATTG 180
Qy 181 TTGCTTAAAGCGCAGAGCGCCAGACCCCACTATATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCTTAAAGCGCAGAGCGCCAGACCCCACTATATAGCCCTATCATTTGCTCAACCC 240
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCAATGTTCTTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCAATGTTCTTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 11
AD136417
ID AD136417 standard; DNA; 307 BP.
XX
AC AD136417;
XX
DT 22-APR-2004 (first entry)
XX
DE DNA encoding the human ADP protein SeqID10.
XX
KW ds; gene; human; prostate; transcriptional response element; TRE;
KW polyethylene glycol; PEG; masking agent; tumour cell growth;
KW proliferation; psoriatic lesion; wound healing; hyperplasia; cancer;
KW cytotatic; antipsoriatic; vulnery; ADP.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 2..307
XX FT /tag= a
XX FT /product= "ADP protein"
XX
XX US2003152553-A1.
XX
XX 14-AUG-2003.
XX
XX 02-MAY-2002; 2002US-00139089.
XX
XX 27-JUN-1995; 95US-00495034.
XX PR 26-JUN-1996; 96US-00669753.
XX PR 03-MAR-1997; 97US-0039597P.
XX PR 03-MAR-1997; 97US-0039762P.
XX PR 03-MAR-1997; 97US-0039763P.
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PR 02-MAR-1998; 98US-00033333.
PR 02-MAR-1998; 98US-00033428.
PR 02-MAR-1998; 98US-00033555.
PR 10-SEP-1998; 98US-00151376.
PR 02-JUN-2000; 2000US-00509591.
XX (LITT/) LITTLE A S.
PA (LAMP/) LAMPARSKI H G.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
XX Little AS, Lamparski HG, Henderson DR, Schuur ER;
XX WPI; 2004-119002/12.
DR P-PSDB; ADI36347.
XX
XX Composition comprising replication competent adenovirus having adenovirus
PT gene essential for replication under transcriptional control of cell type
PT specific transcriptional response element and masking agent.
XX
XX Disclosure; SEQ ID NO 10; 115pp; English.
XX
XX This invention relates to a novel composition that contains a replication
CC competent adenovirus capable of transfecting target host cells.
CC Specifically, it comprises an adenoviral gene essential for replication
CC (E1A, E1B or E4), which is under the transcriptional control of a
CC prostate specific transcriptional response element (TRE) and polyethylene
CC glycol (PEG) as the masking agent. The present invention describes this
CC composition as useful for suppressing tumour cell growth and for lowering
CC the levels of tumour cell markers. It can also be used for introducing
CC transient expression that may be involved in treating undesired
CC proliferations other than tumours, such as psoriatic lesions and wound
CC healing. In addition, it is useful for detecting cells where a cell type-
CC specific TRE is functional in a biological sample and for treating
CC prostate-associated diseases such as hyperplasia and cancer. As such,
CC these compositions exhibit cytostatic, antiproliferative and vulnerary
CC activities. This polynucleotide sequence is the DNA encoding the human
CC ADP protein of the invention. NOTE: This sequence is identical to that
CC given as SeqId 61.
XX
XX Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 12; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGACCGGCTCAACCATCGCGGCCCAACGAGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGGCCCAACGAGACTATCGCAACACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
Qy 121 CATGTGGTGGTTTTCATAGGCGCTTATGTTTGGCTTTATTATTATGTGGCTTATTG 180
Db 121 CATGTGGTGGTTTTCATAGGCGCTTATGTTTGGCTTTATTATTATGTGGCTTATTG 180
Qy 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240
Qy 241 ACACAATGAAAAATTCATAGATTGGAGCGGCTCTGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAATTCATAGATTGGAGCGGCTCTGAAACCATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 12
ADV21029

ID ADV21029 standard; DNA; 307 BP.
XX
AC ADV21029;
XX
XX 24-FEB-2005 (first entry)
DT
XX Human mucin like glycoprotein DF3 (MUC1) TRE DNA.
DE
XX Vector; gene transfer; cloning vehicle; genetic engineering;
XX prostate cancer; gene therapy; vaccine; cytostatic; TRE;
KW transcriptional regulatory element; PSE; prostate specific enhancer; PSA;
KW prostate specific antigen; cancer; ds; mucin like glycoprotein DF3; MUC1.
XX
OS Homo sapiens.
XX
XX US2004241857-A1.
XX
PD 02-DEC-2004.
XX
XX 13-APR-2004; 2004US-00822873.
XX
XX 27-JUN-1995; 95US-00495034.
PR 28-JUN-1996; 96US-00669753.
PR 10-SEP-1998; 98US-00151376.
PR 06-DEC-2000; 2000US-00732169.
XX (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
PA
XX Henderson DR, Schuur ER;
PI
XX WPI; 2005-011642/01.
XX
XX New adenovirus vector comprising an adenovirus early gene essential for
PT propagation under the control of a human prostate specific antigen
PT promoter and a human prostate specific antigen enhancer, for treating
PT prostate cancer.
XX
XX Example 5; SEQ ID NO 61; 112pp; English.
XX
XX The present invention relates to an adenovirus vector comprising an
CC adenovirus early gene essential for propagation under the control of a
CC human prostate specific antigen promoter and a human prostate specific
CC antigen (PSA) enhancer. The invention is useful for treating a patient
CC suffering from prostate cancer and for making mammalian hosts that are
CC transiently transgenic and for detecting the presence of cells that
CC permit the function of a cell type-specific transcriptional regulatory
CC element (TRE) in a sample. The invention is also used in the gene therapy
CC and also as vaccine. The present sequence is the human mucin like
CC glycoprotein DF3 (MUC1)TRE DNA. This sequence is used to construct
CC replication competent prostate-specific attenuated adenoviruses.
XX
XX Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 14; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GATGACCGGCTCAACCATCGCGGCCCAACGAGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGGCCCAACGAGACTATCGCAACACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
Qy 121 CATGTGGTGGTTTTCATAGGCGCTTATGTTTGGCTTTATTATTATGTGGCTTATTG 180
Db 121 CATGTGGTGGTTTTCATAGGCGCTTATGTTTGGCTTTATTATTATGTGGCTTATTG 180
Qy 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240

QY 241 ACACATGAAATTCATAGATTGACGGCTCTGAACCATGTTCTCTTTTACAGTA 300
DB 241 ACACATGAAATTCATAGATTGACGGCTCTGAACCATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 13
ADV20978
ID ADV20978 standard; DNA; 307 BP.
XX
AC ADV20978;
DT 24-FEB-2005 (first entry)
XX
DE Adenovirus death protein (ADP) encoding DNA.
XX
KW Vector; gene transfer; cloning vehicle; genetic engineering;
KW prostate cancer; gene therapy; vaccine; cytostatic;
KW prostate-specific antigen; TRE; transcriptional regulatory element; PSE;
KW prostate specific enhancer; PSA; prostate specific antigen; cancer; ds;
KW ADP; adenovirus death protein; gene.
XX
OS unidentified adenovirus.
XX
FH Key Location/Qualifiers
FT CDS 2..307
FT /*tag= a
FT /product= "Adenovirus death protein (ADP) "

XX US2004241857-A1.
XX
PD 02-DEC-2004.
XX
PF 13-APR-2004; 2004US-00822873.
XX
XX 27-JUN-1995; 95US-00495034.
PR 26-JUN-1996; 96US-00669753.
PR 10-SEP-1998; 98US-00151376.
PR 06-DEC-2000; 2000US-00732169.
XX
XX (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
XX
XX Henderson DR, Schuur ER;
PI
XX WPI; 2005-011642/01.
XX
XX New adenovirus vector comprising an adenovirus early gene essential for
PT propagation under the control of a human prostate specific antigen
PT promoter and a human prostate specific antigen enhancer, for treating
PT prostate cancer.
XX
XX Disclosure; SEQ ID NO 10; 112pp; English.
XX
XX The present invention relates to an adenovirus vector comprising an
CC adenovirus early gene essential for propagation under the control of a
CC human prostate specific antigen promoter and a human prostate specific
CC antigen (PSA) enhancer. The invention is useful for treating a patient
CC suffering from prostate cancer and for making mammalian hosts that are
CC transiently transgenic and for detecting the presence of cells that
CC permit the function of a cell type-specific transcriptional regulatory
CC element (TRE) in a sample. The invention is also used in the gene therapy
CC and also as vaccine. The present sequence is the adenovirus death protein
CC encoding DNA.
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 14; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGGCCCAACGGAATATCGCAACACCACTGCTACCGACT 60
DB 1 GATGACCGGCTCAACCATCGGCCCAACGGAATATCGCAACACCACTGCTACCGACT 60
QY 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCAATGCTTGTCAATGACTGGGCGAGCTTGA 120
DB 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCAATGCTTGTCAATGACTGGGCGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGGCTTATTATTATGTCGCTTATTG 180
DB 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGGCTTATTATTATGTCGCTTATTG 180
QY 181 TTGCTAAAGCGCAGACGGCCAGACCCCCATCTATAGCCCTATCATTTGCTCAACCC 240
DB 181 TTGCTAAAGCGCAGACGGCCAGACCCCCATCTATAGCCCTATCATTTGCTCAACCC 240
QY 241 ACACATGAAATTCATAGATTGACGGCTCTGAACCATGTTCTCTTTTACAGTA 300
DB 241 ACACATGAAATTCATAGATTGACGGCTCTGAACCATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 14
ADM47774
ID ADM47774 standard; DNA; 307 BP.
XX ADM47774;
XX
DT 07-APR-2005 (first entry)
XX
DE Adenovirus death protein coding sequence.
XX
KW Gene therapy; vector; prostate tumor; cytostatic; vasotropic; vulnery;
KW antipsoriatic; antimicrobial; immunomodulator; gene; ds.
XX
OS Human adenovirus type 2.
XX
FH Key Location/Qualifiers
FT CDS 2..307
FT /*tag= a
FT /product= "Adenovirus death protein"
XX
XX WO2005007832-A2.
XX
PD 27-JAN-2005.
XX
XX 24-FEB-2004; 2004WO-US005518.
XX
PR 24-FEB-2003; 2003US-0450232P.
XX
PA (CELL-) CELL GENESYS INC.
XX
XX Harding T, Yu DC;
PI
XX WPI; 2005-102098/11.
DR P-PSDB; ADM47775.
XX
XX New replication competent adenovirus vector comprising an inducible
PT transcriptional transactivator coding sequence and an adenovirus gene,
PT useful for treating cancer, psoriatic lesions, restenosis or wound
PT healing.
XX
XX Disclosure; SEQ ID NO 10; 66pp; English.
XX
XX The present sequence is the coding sequence for adenovirus death protein
CC (ADP). A claimed replication competent adenovirus vector comprises: an
CC inducible transcriptional transactivator (Tt) coding sequence under the
CC transcriptional control of a cell type-specific TRE (Ci-TRE); and an

adenovirus gene under transcriptional control of a TRE regulated by the TT, where the TT is functionally responsive to an exogenous inducer agent. The adenovirus gene is preferably a gene essential for adenoviral replication. The TT may be inhibited or activated by the inducing agent. Also claimed is an adenovirus vector comprising: an inducible TT coding sequence under the transcriptional control of a CT-TRE; and an adenovirus gene under transcriptional control of a TRE regulated by the TT and a second gene under transcriptional control of a second TRE, where the TT is activated by an exogenous inducing agent. The second gene may be an adenoviral gene essential for adenovirus replication, or a transgene such as a cytotoxic gene. One embodiment of the invention provides adenovirus vectors in which an adenovirus gene is under transcriptional control of a first transactivated regulated TRE and a polynucleotide encoding an ADP under control of a second transactivator regulated TRE, where the adenovirus gene is essential for replication. Also claimed are host cells comprising the replication competent adenovirus vector, and methods for propagating and regulating the vector. A claimed method for selective cytolysis of a target tumor cell line involves introducing the adenovirus vector into a cell which allows the CT-TRE to function, and administering an inducing agent such that the adenovirus vector is propagated and causes lysis of target prostate cells. The adenovirus vector can also be used to treat prostatic lesions, restenosis, wound healing, tissue repair, enhanced immune response, resistance to infection, production of factors, enhanced proliferation, investigation of metabolic or other physiological pathways, or comparison of activity of cells in the presence and absence of the virus introduced transgene. In vectors of the invention, expression of a viral gene essential for replication is regulated both by the CT-TRE and the transactivator regulated TRE, and indirectly by the concentration of the inducing agent.

Query Match 100.0%; Score 307; DB 14; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
DB 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
QY 121 CATGTGTGTTTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTTATTG 180
DB 121 CATGTGTGTTTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTTATTG 180
QY 181 TTGCTTAAAGCGCAGCGCGCCAGACCCCATCTATAGGCTTATCATTTGTCTCAACCC 240
DB 181 TTGCTTAAAGCGCAGCGCGCCAGACCCCATCTATAGGCTTATCATTTGTCTCAACCC 240
QY 241 ACACAATGAAAAATTCATAGATTGGAGCGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
DB 241 ACACAATGAAAAATTCATAGATTGGAGCGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 15
ADW28317
ID ADW28317 standard; DNA; 917 BP.
XX AC
XX AC
XX 07-APR-2005 (first entry)
XX Partial DNA sequence of Ad5-yCD/mutTK(SR39)rep-ADP virus (E3 region).
XX chemotherapy; cytosine deaminase; SR39; herpes simplex virus type 1;
KW thymidine kinase; death protein gene; cancer; neoplasm; 5-fluorocytosine;
KW

ganciclovir; Ad5-yCD/mutTK(SR39)rep-ADP; ss.
OS Human adenovirus type 5.
OS Synthetic.
XX WO2005007109-A2.
XX 27-JAN-2005.
XX 09-JUL-2004; 2004WO-US022320.
XX 09-JUL-2003; 2003US-0486219P.
XX (FORD-) FORD HEALTH SYSTEM HENRY.
XX Freytag SD, Kim JH, Barton K, Paielli D;
XX WPI; 2005-101983/11.
XX Novel isolated polynucleotide comprising nucleotide sequence of yeast cytosine deaminase/mutant SR 39 herpes simplex virus type 1 thymidine kinase fusion gene, useful for treating mammalian patient having malignancy or solid tumor.
XX Example; SEQ ID NO 3; 62pp; English.
XX The specification describes a polynucleotide comprising a nucleotide sequence of yeast cytosine deaminase/mutant SR39 herpes simplex virus type 1 thymidine kinase fusion gene, and further comprising an adenovirus type 5 adenovirus death protein gene. The polynucleotide of the invention limits the side effects of cancer treatment by using only lower doses of radiation. The polypeptide encoded by the above polynucleotide is useful for converting 5-fluorocytosine or ganciclovir into active chemotherapeutic agents. Pharmaceutical compositions comprising recombinant adenoviruses comprising polynucleotides of the invention are useful for treating a mammalian patient having a malignancy or solid tumor. The present sequence represents a partial sequence (the E3 region) of a recombinant adenovirus comprising the polynucleotide of the invention. The recombinant adenovirus is designated Ad5-yCD/mutTK(SR39)rep-ADP.

Query Match 100.0%; Score 307; DB 14; Length 917;
Best Local Similarity 100.0%; Pred. No. 4.1e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
DB 422 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 481
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
DB 482 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 541
QY 121 CATGTGTGTTTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTTATTG 180
DB 542 CATGTGTGTTTTCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTTATTG 601
QY 181 TTGCTTAAAGCGCAGCGCGCCAGACCCCATCTATAGGCTTATCATTTGTCTCAACCC 240
DB 602 TTGCTTAAAGCGCAGCGCGCCAGACCCCATCTATAGGCTTATCATTTGTCTCAACCC 661
QY 241 ACACAATGAAAAATTCATAGATTGGAGCGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
DB 662 ACACAATGAAAAATTCATAGATTGGAGCGGTCTGAAACCAATGTTCTCTTTTACAGTA 721
QY 301 TGATTAA 307
DB 722 TGATTAA 728

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 11766282

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Post-processing: Minimum Match 0%

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3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
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12: gb_un.*
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14: gb_htgs.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	307	6	AR137114 Sequence
2	307	100.0	307	6	AR160082 Sequence
3	307	100.0	307	6	BD070679 Adenoviru
4	307	100.0	307	6	BD195488 Adenoviru
5	307	100.0	307	6	BD195538 Adenoviru
6	307	100.0	307	6	BD217928 Adenoviru
7	307	100.0	307	6	BD224262 Adenoviru
8	307	100.0	307	6	AR223335 Sequence
9	307	100.0	307	6	AR349303 Sequence
10	307	100.0	307	6	AR451690 Sequence
11	307	100.0	307	6	AR451740 Sequence
12	307	100.0	307	6	AR474487 Sequence
13	307	100.0	307	6	AR635125 Sequence
14	307	100.0	307	6	AR669908 Sequence
15	307	100.0	3454	13	HAD293912 Human ade
16	307	100.0	3454	13	HAD293914 Human ade
17	307	100.0	3454	13	HAD293916 Human ade
18	307	100.0	3454	13	HAD293917 Human ade

19	307	100.0	35937	6	AX770200	AX770200 Sequence
20	307	100.0	35937	13	ADRCG	J01917 Adenovirus
21	305.4	99.5	3454	13	HAD293913	AJ293913 Human ade
22	305.4	99.5	3454	13	HAD293915	AJ293915 Human ade
c	23	303.8	99.0	34427	6	AR651085 Sequence
24	302.2	98.4	2019	13	ADV16037	Y16037 Adenovirus
25	289.4	94.3	304	6	AX259957	AX259957 Sequence
26	289.4	94.3	304	6	AX259988	AX259988 Sequence
27	289.4	94.3	304	6	AX262362	AX262362 Sequence
28	196	63.8	3776	13	ADSE3	X03002 Adenovirus
29	196	63.8	32166	6	AR628961	AR628961 Sequence
30	196	63.8	33592	6	AX084504	AX084504 Sequence
31	196	63.8	33699	6	AX084506	AX084506 Sequence
32	196	63.8	33988	6	AX084517	AX084517 Sequence
33	196	63.8	34341	6	AX084505	AX084505 Sequence
34	196	63.8	34448	6	AX084507	AX084507 Sequence
35	196	63.8	34737	6	AX084518	AX084518 Sequence
36	196	63.8	35408	6	AR163568	AR163568 Sequence
37	196	63.8	35408	6	AR166442	AR166442 Sequence
38	196	63.8	35724	6	AX084516	AX084516 Sequence
39	196	63.8	35871	6	AR403724	AR403724 Sequence
40	196	63.8	35934	13	AV339865	AY339865 Human ade
41	196	63.8	35935	6	AR091533	AR091533 Sequence
42	196	63.8	35935	6	AR102226	AR102226 Sequence
43	196	63.8	35935	6	AR116313	AR116313 Sequence
44	196	63.8	35935	6	Q0854907	Q0854907 Sequence
45	196	63.8	35935	6	AR230724	AR230724 Sequence

ALIGNMENTS

RESULT 1	AR137114	AR137114	307 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	Sequence	21	from patent US 6197293			
DEFINITION	AR137114					
ACCESSION	AR137114.1	GI:14478623				
VERSION	Unknown.					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 307)					
AUTHORS	Henderson,D.R., Schuur,E.R. and Yu,D.-C.					
TITLE	Adenovirus vectors specific for cells expressing androgen receptor and methods of use thereof					
JOURNAL	Patent: US 6197293-A 21 06-MAR-2001;					
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Db	1	GATGACCGGCTCAACCATCGCGCCCAACGCGACTATCGCAACACCACTCTACCGGACT	60		
Qy	61	AACATCTGCGCTAAATTTACCCCAAGTTTCATGCTTTTGTCATGCTGGCGGAGCTTGA	120		
Db	61	AACATCTGCGCTAAATTTACCCCAAGTTTCATGCTTTTGTCATGCTGGCGGAGCTTGA	120		
Qy	121	CATGCGGTGGTTCATGCGGCTTATGTTTGGCTTATTTATTTATGCGGCTTATTTG	180		
Db	121	CATGCGGTGGTTCATGCGGCTTATGTTTGGCTTATTTATTTATGCGGCTTATTTG	180		
Qy	181	TTGCGCTAAAGCGCAGACGCGCCAGACCCCACTATAGCCTTATCATTTGTCATCAACCC	240		
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Db 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300

Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 2
LOCUS AR160082
DEFINITION Sequence 22 from patent US 6254862.
ACCESSION AR160082
VERSION AR160082.1 GI:16223671
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 307)
  Little,A.S., Henderson,D.R., Schuur,E.R. and Lamparski,H.
  Adenovirus vectors specific for cells expressing alpha-fetoprotein
  and methods of use thereof
  Patent: US 6254862-A 22 03-JUL-2001;
JOURNAL Location/Qualifiers
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  Best Local Similarity 100.0%; Pred. No. 1e-83;
  Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120

Qy 121 CATGTGGTGGTTTCCATAGGCTTATGTTGTTGGCTTATTTATTTATGTCGCTTATTTG 180
Db 121 CATGTGGTGGTTTCCATAGGCTTATGTTGTTGGCTTATTTATTTATGTCGCTTATTTG 180

Qy 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTATCATTTGCTCAACCC 240
Db 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTATCATTTGCTCAACCC 240

Qy 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
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Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 3
LOCUS BD070679
DEFINITION Adenovirus vectors specific for cells expressing androgen receptor
and methods of use thereof.
ACCESSION BD070679
VERSION BD070679.1 GI:22616282
KEYWORDS JP 2001515351-A/21.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
  1 (bases 1 to 307)
  Yu,D.C., Henderson,D.R., Schuur,E.R. and Lamparski,H.G.
  Adenovirus vectors specific for cells expressing androgen receptor
  TITLE
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JOURNAL and methods of use thereof
Patent: JP 2001515351-A 21 18-SEP-2001;
CALYDON INC
COMMENT Unidentified
OS JP 2001515351-A/21
PN 18-SEP-2001
PD 03-MAR-1998 JP 1998538696
PF 03-MAR-1997 US 60/039762,02-MAR-1998 US 09/033333 PI
PR DE CHAO YU,DANIEL R HENDERSON,ERIC R SCHUUR,HENRY G LAMPARSKI PC
DE C12N15/86,C12N5/10,A61K47/00,A61K47/48,C12Q1/70,C12N11/08 CC
Strandedness: Single;
CC Topology: Linear;
CC Adenovirus vectors specific for cells expressing androgen CC
receptor and
CC methods of use thereof
FH Key Location/Qualifiers
FT source 1..307
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FEATURES
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Qy 1 GATGACCGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
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Qy 121 CATGTGGTGGTTTCCATAGGCTTATGTTGTTGGCTTATTTATTTATGTCGCTTATTTG 180
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Qy 181 TTGCTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTATCATTTGCTCAACCC 240
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Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 4
LOCUS BD195488
DEFINITION Adenovirus vectors containing heterologous transcription regulatory
elements and methods of using same.
ACCESSION BD195488
VERSION BD195488.1 GI:33005258
KEYWORDS JP 2002514074-A/9.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
  1 (bases 1 to 307)
  Henderson,D.R., Yu,D.C. and Lamparski,H.G.
  Adenovirus vectors containing heterologous transcription regulatory
  elements and methods of using same
  Patent: JP 2002514074-A 9 14-MAY-2002;
JOURNAL CALYDON INC
COMMENT Unidentified
OS JP 2002514074-A/9
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PD 14-MAY-2002
PF 03-MAR-1998 JP 1998538674
PR 03-MAR-1997 US 60/039762,03-MAR-1997 US 60/039763 PR
04-AUG-1997 US 60/054523,02-MAR-1998 US 09/033556 PI DANIEL
R HENDERSON, DE CHAO YU, HENRY G LAMPARSKI PC
C12N15/86, C12N5/10, A61K48/00, A61K47/48, C12N11/08 CC Strandedness:
Single;
CC Topology: Linear;
CC Adenovirus vectors containing heterologous transcription CC
regulatory
elements and methods of use same
FH Key Location/Qualifiers
FT source 1..307
FT /organism='Unidentified'.
FT Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1e-83;
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QY 1 GATGACGGCTCAACCATCGCGCCCAACGGAATATCGCAACACCACTGCTACCGGACT 60
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QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
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DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATTTATTTATTTGTTG 180
QY 181 TTGCTTAAAGCGCAGACGGCCAGACCCCACTATAGCGCTTATCATTTGTGCTCAACCC 240
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QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 5
BD195538
LOCUS
DEFINITION
BD195538 307 bp DNA linear PAT 17-JUL-2003
Adenovirus vectors specific for cells expressing carcinoembryonic
antigens and methods of use thereof.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 307)
Lamparski, H.G., Henderson, D.R. and Schuur, E.R.
Adenovirus vectors specific for cells expressing carcinoembryonic
antigens and methods of use thereof
Patent: JP 2002514075-A 19 14-MAY-2002;
CALYDON INC
OS Unidentified
PN JP 2002514075-A/19
PD 14-MAY-2002
PF 03-MAR-1998 JP 1998538697
PR 03-MAR-1997 US 60/039763,02-MAR-1998 US 60/039763 PI
HENRY G LAMPARSKI, DANIEL R HENDERSON, ERIC R SCHUUR PC

C12N15/86, C12N5/10, A61K48/00, A61K47/48, C12Q1/70, C12N11/08 CC
Strandedness: Double;
CC Topology: Linear;
CC Adenovirus vectors specific for cells expressing CC
carcinoembryonic antigens
CC and methods of use thereof
FH Key Location/Qualifiers
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FT Location/Qualifiers
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QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATTTATTTATTTGTTG 180
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QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
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QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 6
BD217928
LOCUS
DEFINITION
BD217928 307 bp DNA linear PAT 17-JUL-2003
Adenovirus vector specific to cell expressing alpha-fetoprotein and
method of using the same.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 307)
Little, A.S., Lamparski, H.G., Henderson, D.R. and Schuur, E.R.
Adenovirus vector specific to cell expressing alpha-fetoprotein and
method of using the same
Patent: JP 2002516568-A 22 04-JUN-2002;
CALYDON INC
OS Artificial Sequence
PN JP 2002516568-A/22
PD 04-JUN-2002
PF 03-MAR-1998 JP 1998538676
PR 03-MAR-1997 US 60/039597,02-MAR-1998 US 09/033428 PI
ANDREW S LITTLE, HENRY G LAMPARSKI, DANIEL R HENDERSON, ERIC R PI
SCHUUR
PC C12N15/86, C12N7/00
CC Nucleotide Sequence for ADP
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Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGTGCTCAACCC 240

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Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 8
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LOCUS AR223335 307 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 21 from patent US 6436394.
ACCESSION AR223335
VERSION AR223335.1 GI:233331486
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 307)
  Henderson,D.R., Schuur,E.R. and Yu,D.-C.
  Adenovirus vectors specific for cells expressing androgen receptor
  and methods of use thereof
  Patent: US 6436394-A 21-20-AUG-2002;
  Cell Genesys, Inc.; Foster City, CA
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Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120
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Qy 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTGTTGGCTTATTATTATGTTGGCTTATTG 180
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Qy 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGTGCTCAACCC 240
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Db 301 TGATTAA 307

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Db 301 TGATTAA 307

RESULT 7
BD224262
LOCUS BD224262 307 bp DNA linear PAT 17-JUL-2003
DEFINITION Adenovirus vectors containing cell status-specific response
elements and methods of use thereof.
ACCESSION BD224262
VERSION BD224262.1 GI:33034032
KEYWORDS JP 2002525063-A/8.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE
  1 (bases 1 to 307)
  Yu,D.C. and Henderson,D.R.
  Adenovirus vectors containing cell status-specific response
  elements and methods of use thereof
  Patent: JP 2002525063-A 8 13-AUG-2002;
  CALYDON INC
COMMENT
  OS Adenovirus V
  PN JP 2002525063-A/8
  PD 13-AUG-2002
  PF 10-SEP-1999 JP 2000570347
  PR 10-SEP-1998 US 60/099791,09-SEP-1999 US 09/392822 PI
  DE CHAO YU,DANIEL R HENDERSON
  PC
  C12N15/09,A61K48/00,A61P35/00,C12N1/15,C12N1/19,C12N1/21,C12N5/PC
  10,
  PC C12N7/02//A61K35/76,C12N15/00,C12N5/00
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  elements and
  CC methods of use thereof
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Db 301 TGATTAA 307

RESULT 9
LOCUS AR349303
DEFINITION Sequence 22 from patent US 6585968.
ACCESSION AR349303
VERSION AR349303.1 GI:33750029
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Little,A.S., Henderson,D.R., Schuur,E.R. and Lamparski,H.
TITLE Adenovirus vectors specific for cells expressing alpha-fetoprotein
and methods of use thereof
JOURNAL Patent: US 6585968-A 22 01-JUL-2003;
Cell Genesys, Inc.; Foster City, CA
FEATURES
source Location/Qualifiers
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QY 301 TGATTAA 307
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Db 301 TGATTAA 307

RESULT 11
LOCUS AR451740
DEFINITION Sequence 61 from patent US 6676935.
ACCESSION AR451740
VERSION AR451740.1 GI:42682855
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Henderson,D.R. and Schuur,E.R.
TITLE Tissue specific adenoviral vectors
JOURNAL Patent: US 6676935-A 61 13-JAN-2004;
Cell Genesys, Inc.; South San Francisco, CA
FEATURES
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ORIGIN
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QY 301 TGATTAA 307
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Db 301 TGATTAA 307

RESULT 10
LOCUS AR451690
DEFINITION Sequence 10 from patent US 6676935.
ACCESSION AR451690
VERSION AR451690.1 GI:42682805
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Henderson,D.R. and Schuur,E.R.
TITLE Tissue specific adenoviral vectors

JOURNAL Patent: US 6676935-A 10 13-JAN-2004;
Cell Genesys, Inc.; South San Francisco, CA
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QY 301 TGATTAA 307
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Db 301 TGATTAA 307

RESULT 11
LOCUS AR451740
DEFINITION Sequence 61 from patent US 6676935.
ACCESSION AR451740
VERSION AR451740.1 GI:42682855
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Henderson,D.R. and Schuur,E.R.
TITLE Tissue specific adenoviral vectors
JOURNAL Patent: US 6676935-A 61 13-JAN-2004;
Cell Genesys, Inc.; South San Francisco, CA
FEATURES
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Db 301 TGATTAA 307

RESULT 12
AR474487
LOCUS AR474487 307 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 17 from patent US 6692736.
ACCESSION AR474487
VERSION AR474487.1 GI:42713368
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Yu D.-C., Li, Y., Little, A. S. and Henderson, D. R.
TITLE Cell-specific adenovirus vectors comprising an internal ribosome
entry site
JOURNAL Patent: US 6692736-A 17 FEB-2004;
Cell Genesys, Inc.; South San Francisco, CA
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AR635125
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DEFINITION Sequence 3 from patent US 6852528.
ACCESSION AR635125
VERSION AR635125.1 GI:59793252
KEYWORDS
SOURCE Unknown.
Qy 181 TTGCCTAAAGCGCAGCGCCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240
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AR669908
LOCUS AR669908 307 bp DNA linear PAT 13-JUN-2005
DEFINITION Sequence 7 from patent US 6900049.
ACCESSION AR669908
VERSION AR669908.1 GI:67608182
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Yu, D. C. and Henderson, D. R.
TITLE Adenovirus vectors containing cell status-specific response
elements and methods of use thereof
JOURNAL Patent: US 6900049-A 7 31-MAY-2005;
Cell Genesys, Inc.; San Francisco, CA
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Query Match 100.0%; Score 307; DB 6; Length 307;
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Qy 301 TGATTAA 307
Db 301 TGATTAA 307

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Yu, D.-C., Zhang, H. and Henderson, D. R.
TITLE Human and mouse uroplakin II gene transcriptional regulatory
elements
JOURNAL Patent: US 6852528-A 3 08-FEB-2005;
Cell Genesys, Inc.; San Francisco, CA
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Db 301 TGATTAA 307
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RESULT 15
LOCUS HAD293912 3454 bp DNA linear VRL 15-APR-2005
DEFINITION Human adenovirus type 2 early E3 region, isolate R05.
ACCESSION AJ293912
VERSION Au293912.1 GI:15485529
KEYWORDS 10.4K protein; 11.6K protein; 12.5K protein; 14.5K protein; 14.7K protein; 19K glycoprotein; 6.7K protein; L4 protein VIII; protein VII gene.
SOURCE Human adenovirus type 2
ORGANISM Human adenovirus type 2
REFERENCE 1
1 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
Borcherding, F. and Pring-Akerblom, P.
TITLE Adenoviruses of subgenus C with different organ tropism
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3454)
Borcherding, F.
AUTHORS Direct Submission
TITLE Submitted (01-SEP-2000) Borcherding F., Institut fuer Virologie,
JOURNAL Medizinische Hochschule Hannover, Carl-Neuberg-Str. 1, 30625 Hannover, GERMANY
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Best Local Similarity 100.0%; Pred. No. 1.2e-83;
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QY 1 GATGACCGGCTCAACCATCGGCCCAACACGAGCTATCGCAACACCATGCTACCGGACT 60
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Qy	241	ACACAAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA	300
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